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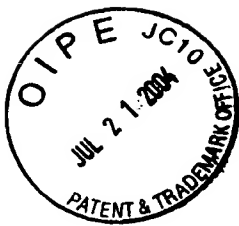
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5'	9	18	27	36	45	54
GGC CTG CTG CTG ACC TAC CTG CTC CCT CTG CTG GTC ATC CTC CTG TCT TAC						
---	---	---	---	---	---	---
Gly Leu Leu Leu Val Thr Tyr Leu Leu Pro Leu Leu Val Ile Leu Leu Ser Tyr						
	63	72	81	90	99	108
GTC CGG GTG TCA GTG AAG CTC CGC AAC CGC CTG CTG CCG GGC TGC GTG ACC CAG						
---	---	---	---	---	---	---
Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly Cys Val Thr Gln						
	117	126	135	144	153	162
AGC CAG GCC GAC TGG GAC CGC GCT CGG CGC CGG CGC ACC TTC TGC TTG CTG GTG						
---	---	---	---	---	---	---
Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg Thr Phe Cys Leu Leu Val						
	171	180	189	198		
GTG GTC GTG GTG TTT GCC ATC TGC TGG TTG CCT TAC TAC 3'						
---	---	---	---	---	---	---
Val Val Val Val Val Phe Ala Ile Cys Trp Leu Pro Tyr Tyr						

FIG. 2

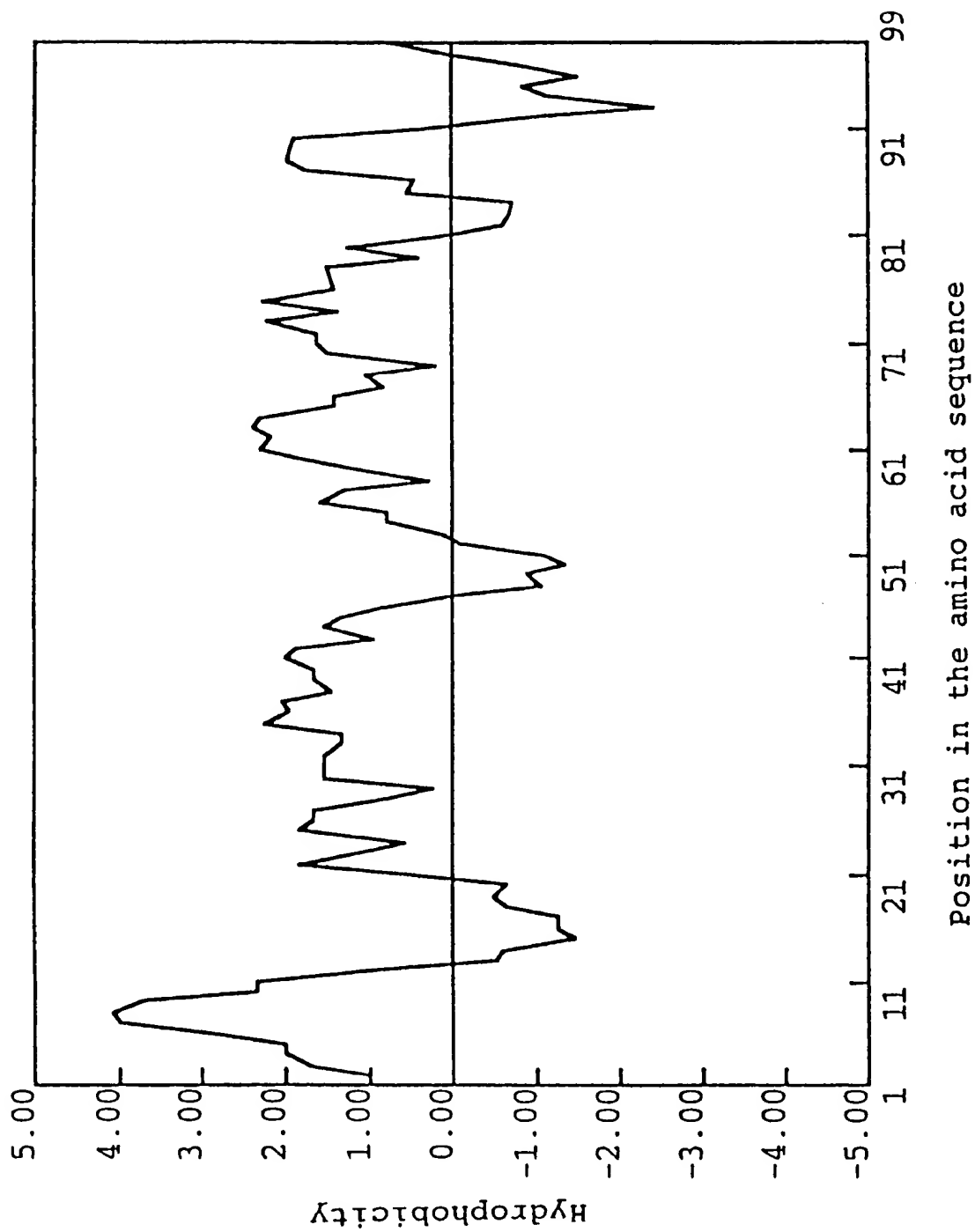


FIG. 3

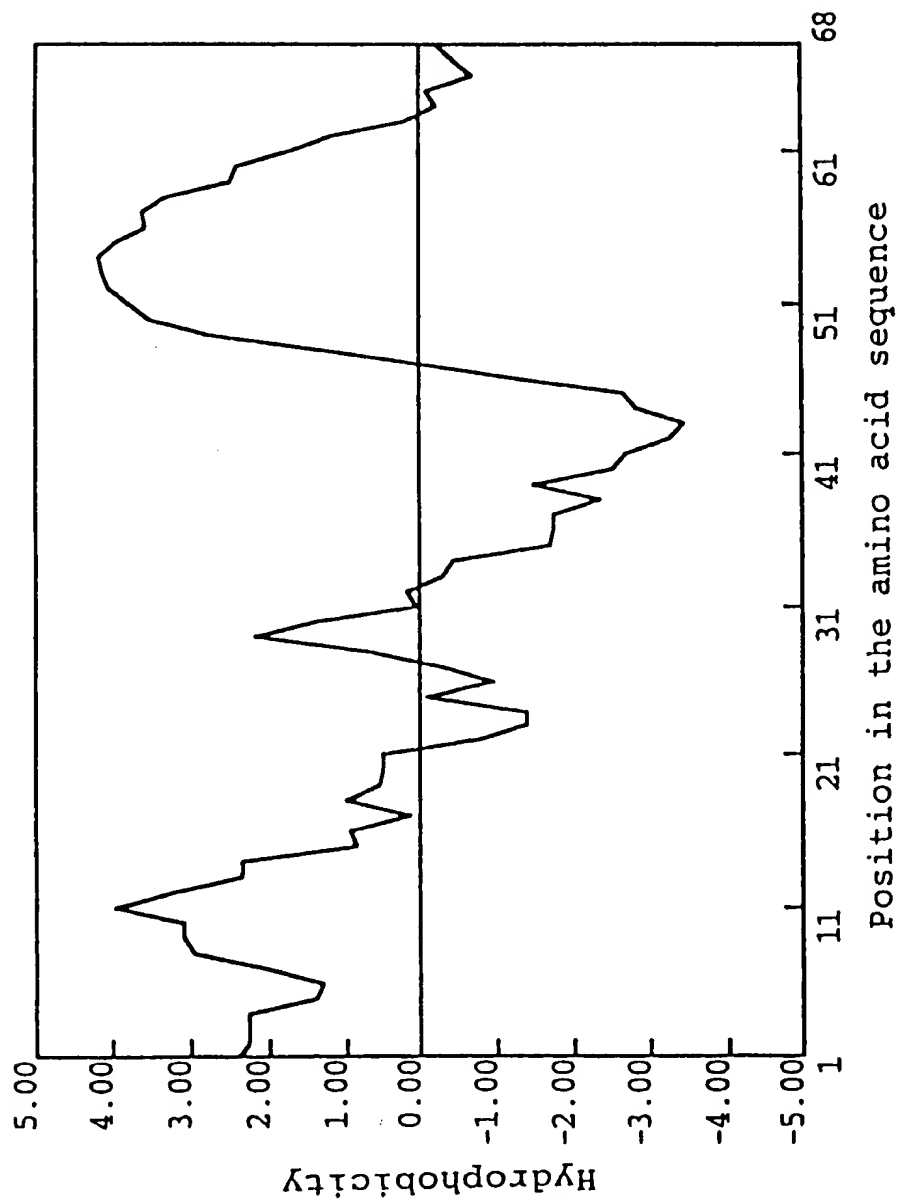
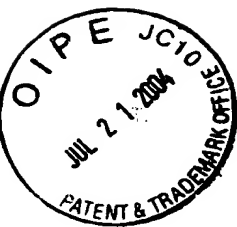


FIG. 4



FIG. 5

FIG. 6A
FIG. 6B
FIG. 6C

FIG. 6

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5'	9	GTG	GGC	ATG	GTG	GGC	AAC	ATC	CTG	CTG	CTG	CTG	ATC	GGC	CGG	CTG	CGC	CGG	54
		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
		Val	Gly	Met	Val	Gly	Asn	Ile	Leu	Leu	Val	Val	Ile	Ala	Arg	Val	Arg	Arg	
	63	CTG	TAC	AAC	GTG	ACG	AAT	TTC	CTC	ATC	GGC	AAC	CTG	GGC	TTC	GAC	GTG	CTC	108
		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
		Leu	Tyr	Asn	Val	Thr	Asn	Phe	Leu	Ile	Gly	Asn	Leu	Ala	Leu	Ser	Asp	Val	Leu
	117	ATG	TGC	ACC	GGC	TGC	GTG	CCG	CTC	ACG	CTG	GGC	TAT	GGC	TTC	GAG	CCA	CGC	GGC
		---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	
		Met	Cys	Thr	Ala	Cys	Val	Pro	Leu	Thr	Leu	Ala	Tyr	Ala	Phe	Glu	Pro	Arg	Gly

FIG. 6A

171	180	189	198	207	216
TGG GTG TTC GGC GGC CTG TGC CAC CTC TTC CTC CAG GCG GTC ACC					
---	---	---	---	---	---
Trp Val Phe Gly Gly Leu Cys His Leu Val Phe Phe Leu Gln Ala Val Thr					
225	234	243	252	261	270
GTC TAT GTG TCG GTG TTC ACG CTC ACC ACC ATC GCA GTG GAC CGC TAC GTC GTG					
---	---	---	---	---	---
Val Tyr Val Ser Val Phe Thr Leu Thr Thr Thr Ile Ala Val Asp Arg Tyr Val Val					
279	288	297	306	315	324
CTG GTG CAC CCG CTG AGG CCG CGC ATC TCG CTG CGC CTC AGC GCC TAC GCT GTG					
---	---	---	---	---	---
Leu Val His Pro Leu Arg Arg Arg Ile Ser Leu Arg Leu Ser Ala Tyr Ala Val					
333	342	351	360	369	378
CTG GCC ATC TGG GTG CTG TCC GCG GTG CTG GCG CTC CCC GCC GTC CAC ACC					
---	---	---	---	---	---
Leu Ala Ile Trp Val Leu Ser Ala Val Leu Ala Leu Pro Ala Ala Val His Thr					
387	396	405	414	423	432
TAT CAC GTG GAG CTC AAG CCG CAC GAC GTG GCG CTC TGC GAG GAG TTC TGG GGC					
---	---	---	---	---	---
Tyr His Val Glu Leu Lys Pro His Asp Val Arg Leu Cys Glu Phe Trp Gly					

FIG. 6B



441	TCC	CAG	GAG	CGC	CAG	CGC	CAG	CTC	TAC	GCC	TGG	GGG	CTG	CTG	CTG	477	486
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	TAC
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
---	Ser	Gln	Glu	Arg	Gln	Arg	Gln	Leu	Tyr	Ala	Trp	Gly	Leu	Leu	Val	Thr	Tyr
495	CTG	CTC	CCT	CTG	CTG	GTC	ATC	CTC	CTG	TCT	TAC	GCC	CGG	GTG	GTG	531	540
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	CTC
---	Leu	Leu	Pro	Leu	Leu	Val	Ile	Leu	Leu	Ser	Tyr	Ala	Arg	Val	Ser	Val	Lys
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	Leu
549	CGC	AAC	CGC	GTG	GTG	CCG	CGC	CGC	GTG	ACC	CAG	AGC	CAG	GCC	GAC	585	594
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	CGC
---	Arg	Asn	Arg	Val	Val	Pro	Gly	Arg	Val	Thr	Gln	Ser	Gln	Ala	Asp	Trp	Arg
603	CCT	CGG	CGG	CGG	ACC	612	TTC	TGC	TTC	CTG	GTG	GTG	GTG	GTG	GTG	639	648
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	ACC
---	Ala	Arg	Arg	Arg	Thr	Thr	Phe	Cys	Leu	Leu	Val	Val	Val	Val	Val	Val	Thr
657	CTC	TGC	TGG	CTG	CCC	666	TTC	TTC	3'	---	---	---	---	---	---	---	---
---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---	---
---	Leu	Cys	Trp	Leu	Pro	Pro	Phe	Phe	---	---	---	---	---	---	---	---	---

FIG. 6C



FIG. 7

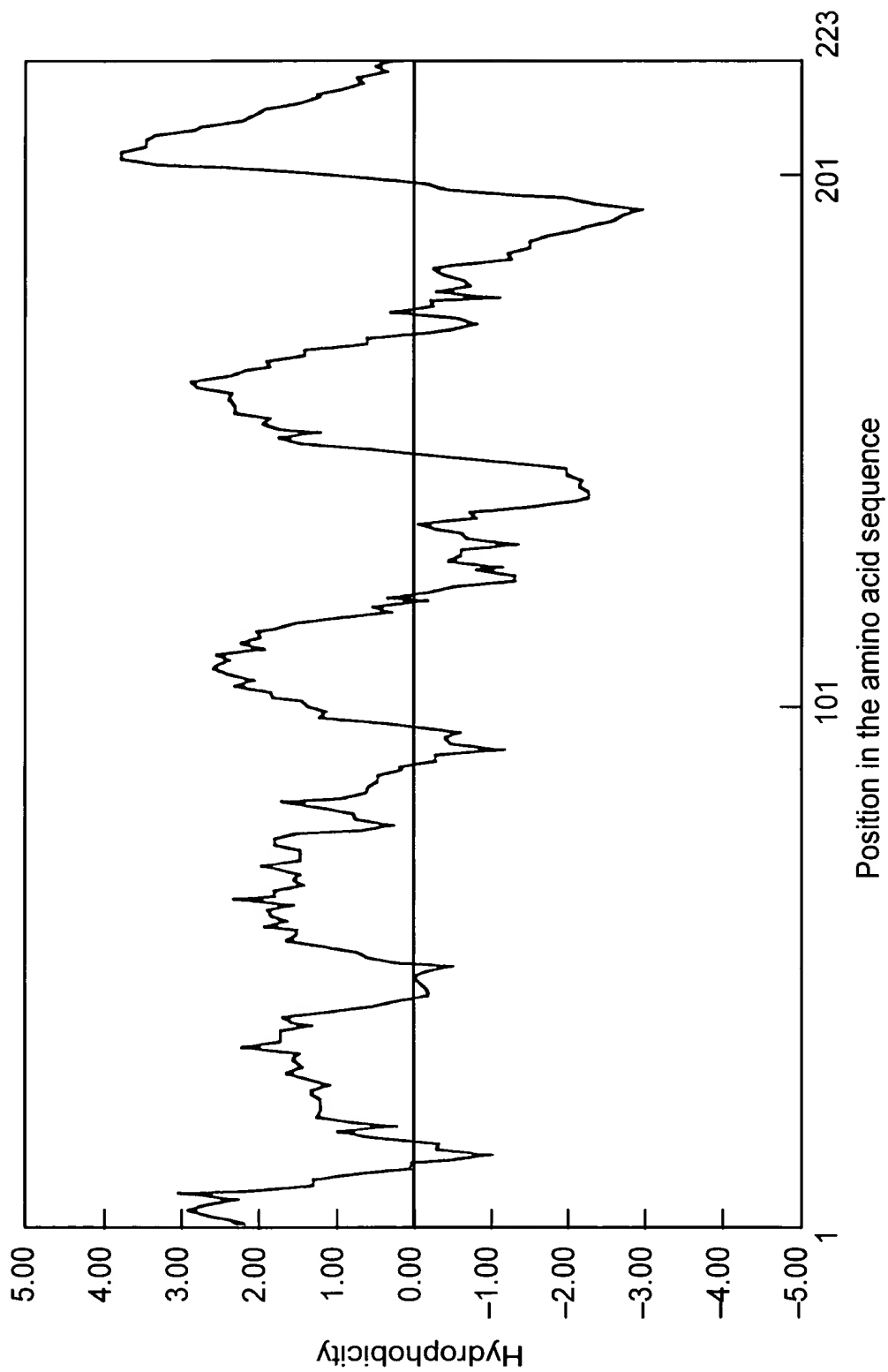


FIG. 8

FIG. 9A
FIG. 9B
FIG. 9C

# FIG. 9

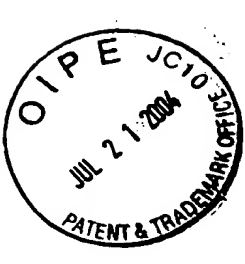
1 CATCGTCAAGCAGATGAAGATCATCCACGAGGATCGCTACTCCGAGGCCAGCAGAAATT 60  
1  
61 CTGCCCCCTTCTTCCCGCGAGTGCTTTCCCGCTCTCCAAACCCCACTCCAGGTGCCCATG 120  
1 Met 1  
121 GCCTCATCGACCACTCGGGGCCCCAGGGTTTCTGACTTATTTTCTGGGCTGCCGCCGGCG 180  
1 AlaSerSerThrThrArgGlyProArgValSerAspLeuPheSerGlyLeuProProAla 21  
181 GTCACAACTCCCGCCAACCAAGCGCAGAGGCCCTCGCGGGCAACGGGTGCGTGGCTGGC 240  
21 ValThrThrProAlaAsnGlnSerAlaGluAlaSerAlaGlyAsnGlySerValAlaGly 41  
241 GCGGACGCTCCAGCCGTACGCCCTTCCAGAGCCTGCAGCTGGTGCATCAGCTGAAGGG 300  
41 AlaAspAlaProAlaValThrProPheGlnSerLeuGlnLeuValHisGlnLeuLysGly 61

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## FIG. 9A

301	CTGATCGTCTCTACAGCGTCTGTCGTCGTCGGCTGTCGGCAACTGCCCTGCTG	360
61	LeuIleValLeuLeuTyrSerValValValValValGlyLeuValGlyAsnCysLeuLeu	81
361	GTGCTGGTATCGCGGGTGGCGCGGTGCACAACGTGACGAACCTTCCTCATCGCAAC	420
81	ValLeuValIleAlaArgValArgArgLeuHisAsnValThrAsnPheLeuIleGlyAsn	101
421	CTGGCCTTGTCCGACGTGCTCATGTGCACCGCCTGCGTGCCGCTCAGCGTGGCCTATGCC	480
101	LeuAlaLeuSerAspValLeuMetCysThrAlaCysValProLeuThrLeuAlaTyrAla	121
481	TTCGAGCCACGCGGTGGTGTTCGGCGCGGCTGTGCCACCTGGTCTTCTTCCTGCAG	540
121	PheGluProArgGlyTrpValPheGlyGlyLeuCysHisLeuValPhePheLeuGln	141
541	CCGTCACCGTCTATGTGTGTCGGTGTTCACGCTCACCATCCAGTCGACCGCTACGTC	600
141	ProValThrValTyrValSerValPheThrLeuThrThrIleAlaValAspArgTyrVal	161
601	GTGCTGGTGCACCGCTGAGCGCGGCATCTCGCTGCGCCTCAGCGCCTACGCTGTGCTG	660
161	ValLeuValHisProLeuArgArgIleSerLeuArgLeuSerAlaTyrAlaValLeu	181
661	GCCATCTGGCGCTGTCCGCGTGTGCGGCTGCCCGCGCGTGCACACCTATCACGTC	720
181	AlaIleTrpAlaLeuSerAlaValLeuAlaLeuProAlaAlaValHisThrTyrHisVal	201
721	GAGCTCAAGCCGACGACGTGCGCCTCTGCGAGGAGTTCTGGGGTCCAGGAGCGCCAG	780
201	GluLeuLysProHisAspValArgLeuCysGluGluPheTrpGlySerGlnGluArgGln	221
781	CGCCAGCTCTACGCGCTGGGGGCTGCTGTCGTACCTACCTGCTCCCTCTGCTGTCATC	840
221	ArgGlnLeuTyrAlaTrpGlyLeuLeuLeuValThrTyrLeuLeuProLeuLeuValIle	241

FIG. 9B



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841	CTCCTGTCTTACGTCGGGTGTCAGTGAAGCTCCGCAACCGGTGGTCCGGCTGCGTG	900
241	LeuLeuSerTyrValArgValSerValLysLeuArgAsnArgValValProGlyCysVal	261
901	ACCCAGAGCCAGCCGACTGGGACCGCGCTCGCGCCGCGCACCTTCTGCTTGTCTGGTG	960
261	ThrGlnSerGlnAlaAspTrpAspArgAlaArgArgArgThrPheCysLeuLeuVal	281
961	GTGGTCGTGGTGTTCGCCGTCTGCTGGCTGCCGTGCACGTCTTCAACCTGCTGCCG	1020
281	ValValValValPheAlaValCysTrpLeuProLeuHisValPheAsnLeuLeuArg	301
1021	GACCTCGACCCCAACGCAATCGACCCCTTACGCCCTTTGGCTGGTGCAGCTGCTGCCAC	1080
301	AspLeuAspProHisAlaIleAspProTyrAlaPheGlyLeuValGlnLeuLeuCysHis	321
1081	TGGCTCGCCATGAGTTTCGGCTGTCTACAACCCCTTCACTCTACGCCCTGGCTGCACGACGC	1140
321	TrpLeuAlaMetSerSerAlaCysTyrAsnProPheIleTyrAlaTrpLeuHisAspSer	341
1141	TTCCCGGAGGAGCTGCGCAACTGTTGGTGGCTTGGCCCCCGCAAGATAGCCCCCATGGC	1200
341	PheArgGluGluLeuArgLysLeuLeuValAlaTrpProArgLysIleAlaProHisGly	361
1201	CAGAAATATGACCGTCAGCGTGGTCACTCTGATGCCACTTAGCCAGGCCCTTGGTCAAGGAGC	1260
361	GlnAsnMetThrValSerValValIle***	371
1261	TCCACTTCAACTGGCCTCCTAGCGCACCACTCGAGGTCAATCTGCTTATTCTCAGCA	1320
	371	371
1321	CCAGAGCTAGC	1331
	371	371

FIG. 9C

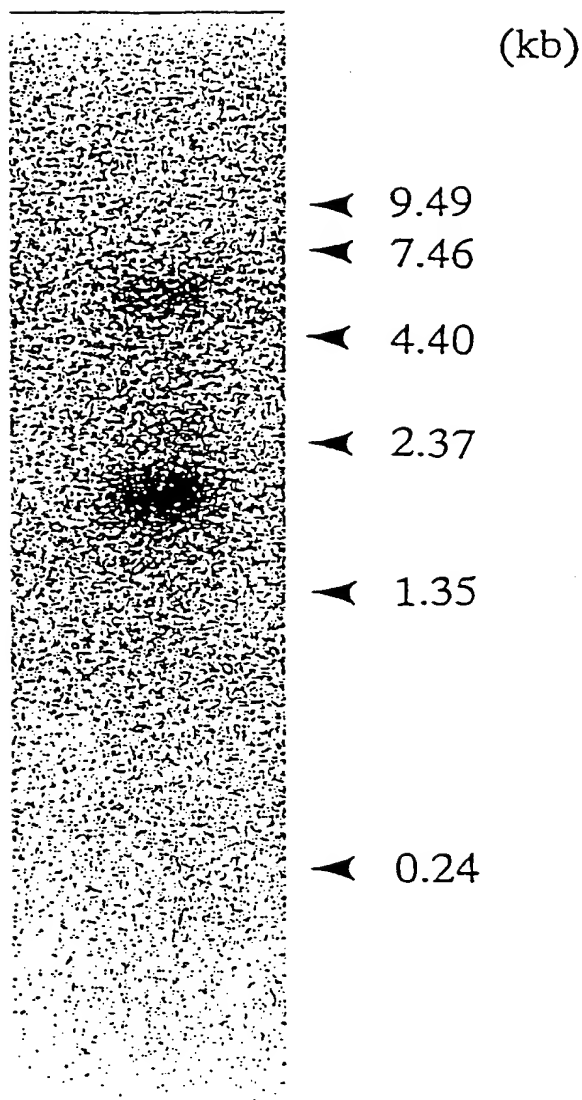


FIG. 10

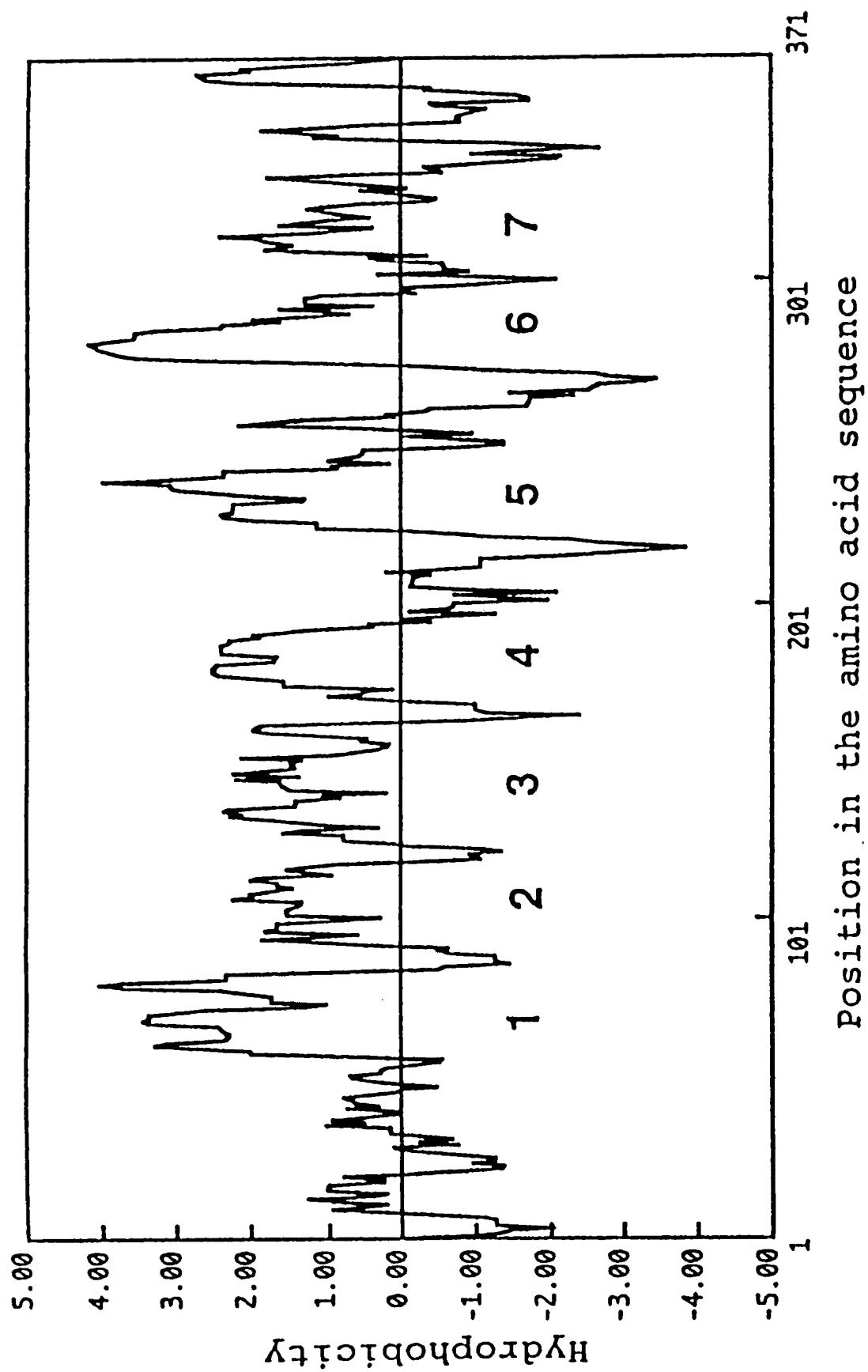
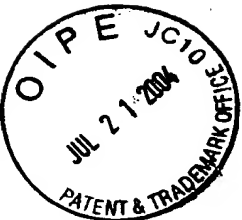


FIG. 11





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5'                    9                    18                    27                    36                    45                    54  
 CTG TGT GTC ATC GCG GTG GAT AGG TAC GTG GTT CTG GTG CAC CCG CTA CGT CGG  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
Leu Cys Val Ile Ala Val Asp Arg Tyr Val Val Leu Val His Pro Leu Arg Arg

                  63                    72                    81                    90                    99                    108  
 CGC ATT TCA CTG AGG CTC AGC GCC TAC GCG GTG CTG GGC ATC TGG GCT CTA TCT  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 Arg Ile Ser Leu Arg Leu Ser Ala Tyr Ala Val Leu Gly Ile Trp Ala Leu Ser

                  117                    126                    135                    144                    153                    162  
 GCA GTG CTG GCG CTG CCG GCC GCG GTG CAC ACC TAC CAT GTG GAG CTC AAG CCC  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 Ala Val Leu Ala Leu Pro Ala Ala Val His Thr Tyr His Val Glu Leu Lys Pro

                  171                    180                    189                    198                    207                    216  
 CAC GAC GTG AGC CTC TGC GAG GAG TTC TGG GGC TCG CAG GAG CCG CAA CGC CAG  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 His Asp Val Ser Leu Cys Glu Glu Phe Trp Gly Ser Gln Glu Arg Gln Arg Gln

                  225                    234                    243                    252                    261                    270  
 ATC TAC GCC TGG GGG CTG CTT CTG GGC ACC TAT TTG CTC CCC CTG CTG GCC ATC  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 Ile Tyr Ala Trp Gly Leu Leu Leu Gly Thr Tyr Leu Leu Pro Leu Leu Ala Ile

                  279                    288                    297                    306                    315                    324  
 CTC CTG TCT TAC GTA CGG GTG TCA GTG AAG CTG AGG AAC CGC GTG GTG CCT GGC  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu Arg Asn Arg Val Val Pro Gly

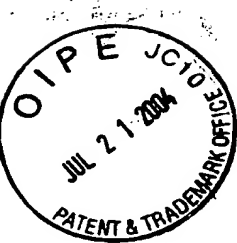
                  333                    342                    351                    360                    369                    378  
 AGC GTG ACC CAG AGT CAA GCT GAC TGG GAC CGA GCG CGT CGC CGC CGC ACT TTC  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 Ser Val Thr Gln Ser Gln Ala Asp Trp Asp Arg Ala Arg Arg Arg Arg Thr Phe

                  387                    396                    405                    414                    423                    432  
 TGT CTG CTG GTG GTG GTG GTG GTA GTG TTC ACG CTC TGC TGG CTG CCC TTC TAC  
 --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---  
 Cys Leu Leu Val Val Val Val Val Val Phe Thr Leu Cys Trp Leu Pro Phe Tyr

CT 3'

--  
 —

FIG. 12



p19P2	1	VGMVGNVLLV	10	LVIARVRRLLH	20	NVTNFLIGNL	30	ALSDVLMCTA	40	CVPLTLAYAF	50	
pG3-2/pG1-10	1	VGMVGNVLLV		LVIARVRRLLY		NVTNFLIGNL		ALSDVLMCTA		CVPLTLAYAF		50
p5S38	-79											-30
p19P2	51	EPRGMVFCGG	60	LCHLVFFLQp	70	VTVVVSVFTL	80	TTIAVDRYVV	90	LVHPLRRRI-	100	
pG3-2/pG1-10	51	EPRGMVFCGG		LCHLVFFLQA		VTVVVSVFTL		TTIAVDRYVV		LVHPLRRRIIS		100
p5S38	-29							CVIAVDRYVV		LVHPLRRRIIS		21
p19P2	101		110		120		130		140		150	
pG3-2/pG1-10	101	LRLSAYAVLA		IWL SAVLAL		PAAVHTYHVE		LKPHDVRICE		EFWGSQERQR		150
p5S38	22	LRLSAYAVLG		IWA SAVLAL		PAAVHTYHVE		LKPHDVSICE		EFWGSQERQR		71
p19P2	151		160		170		180		190		200	
pG3-2/pG1-10	151	GLLLV		TYLLPLLVIL		LSYVRVSVKL		RNRVVPGCVT		QSQADWDRAR		200
p5S38	72	QIYANGLLLG		TYLLPLLVIL		LSYVRVSVKL		RNRVVPGRVT		QSQADWDRAR		200
				TYLLPLLAII		LSYVRVSVKL		RNRVVPGSVT		QSQADWDRAR		121
p19P2	201	RRRTFCLLV	210	VVVVFALCML	220	PFY	230		240		250	
pG3-2/pG1-10	201	RRRTFCLLV		VVVVFTLCML		PFF						250
p5S38	122	RRRTFCLLV		VVVVFTLCML		PFY						171

FIG. 13

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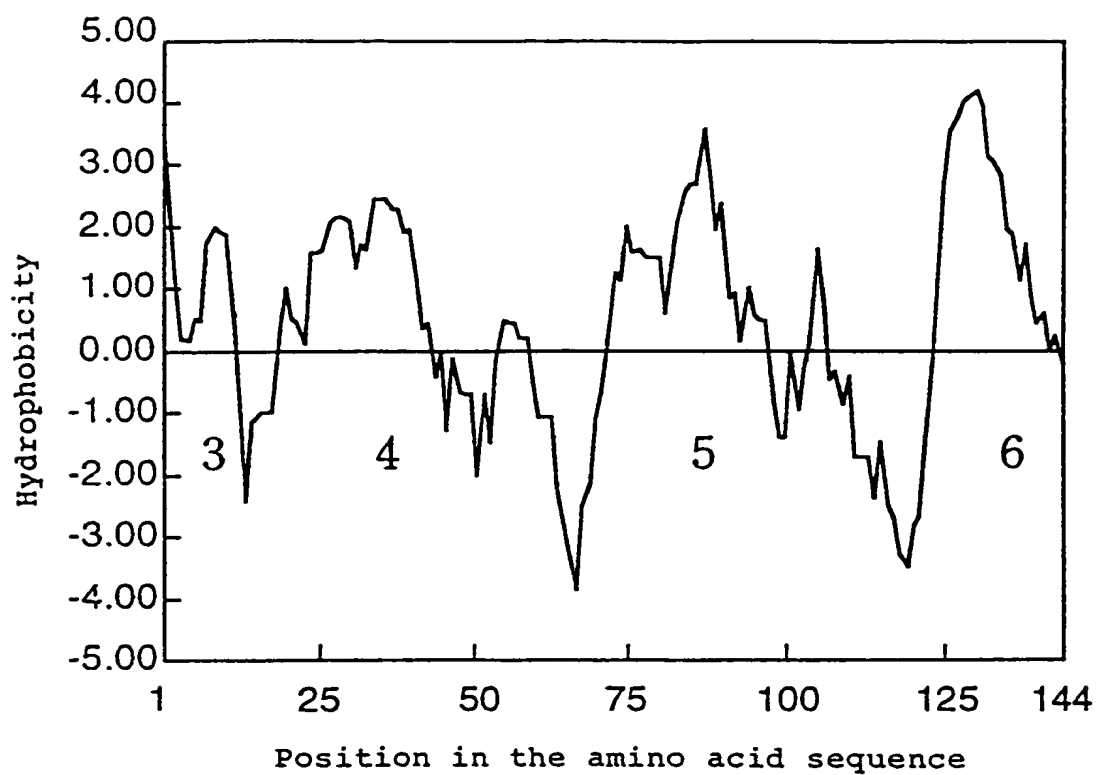


FIG. 14

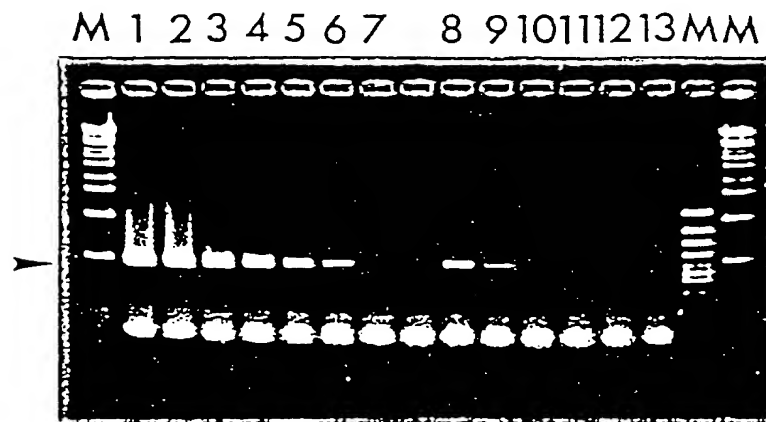


FIG. 15

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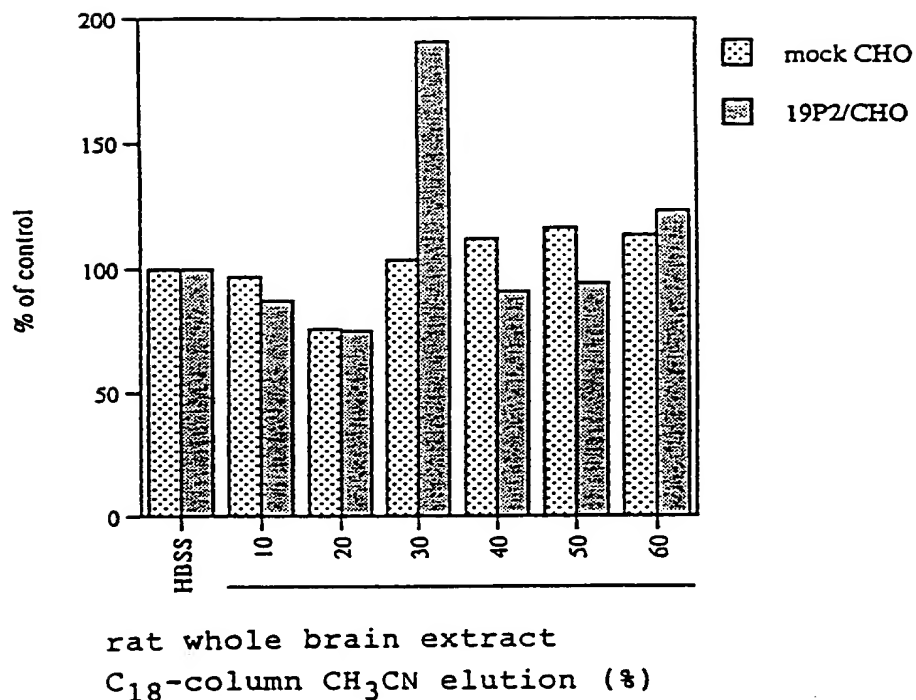


FIG. 16

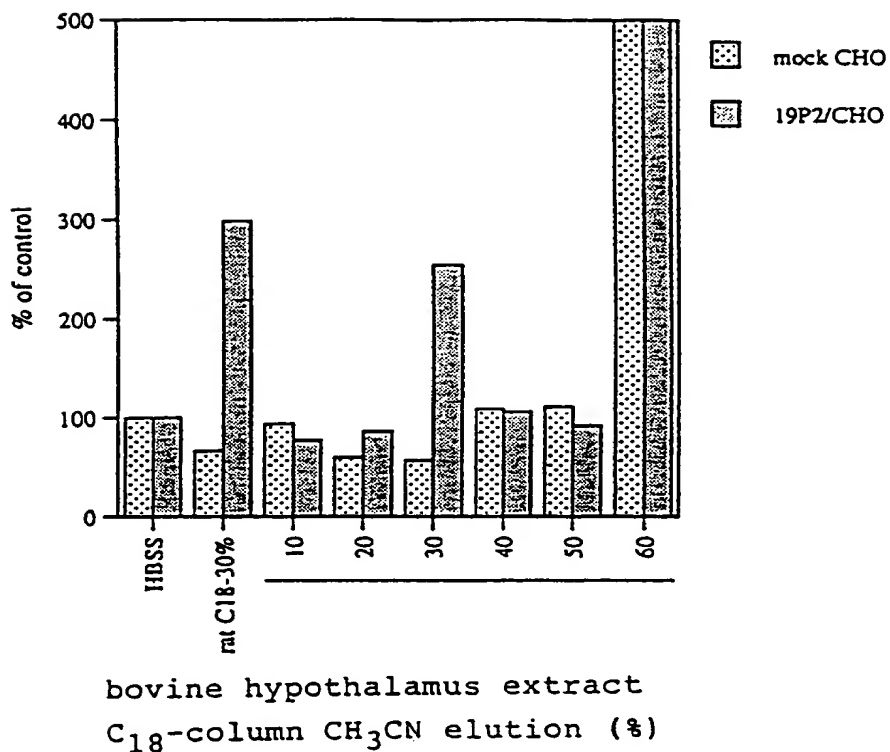


FIG. 17

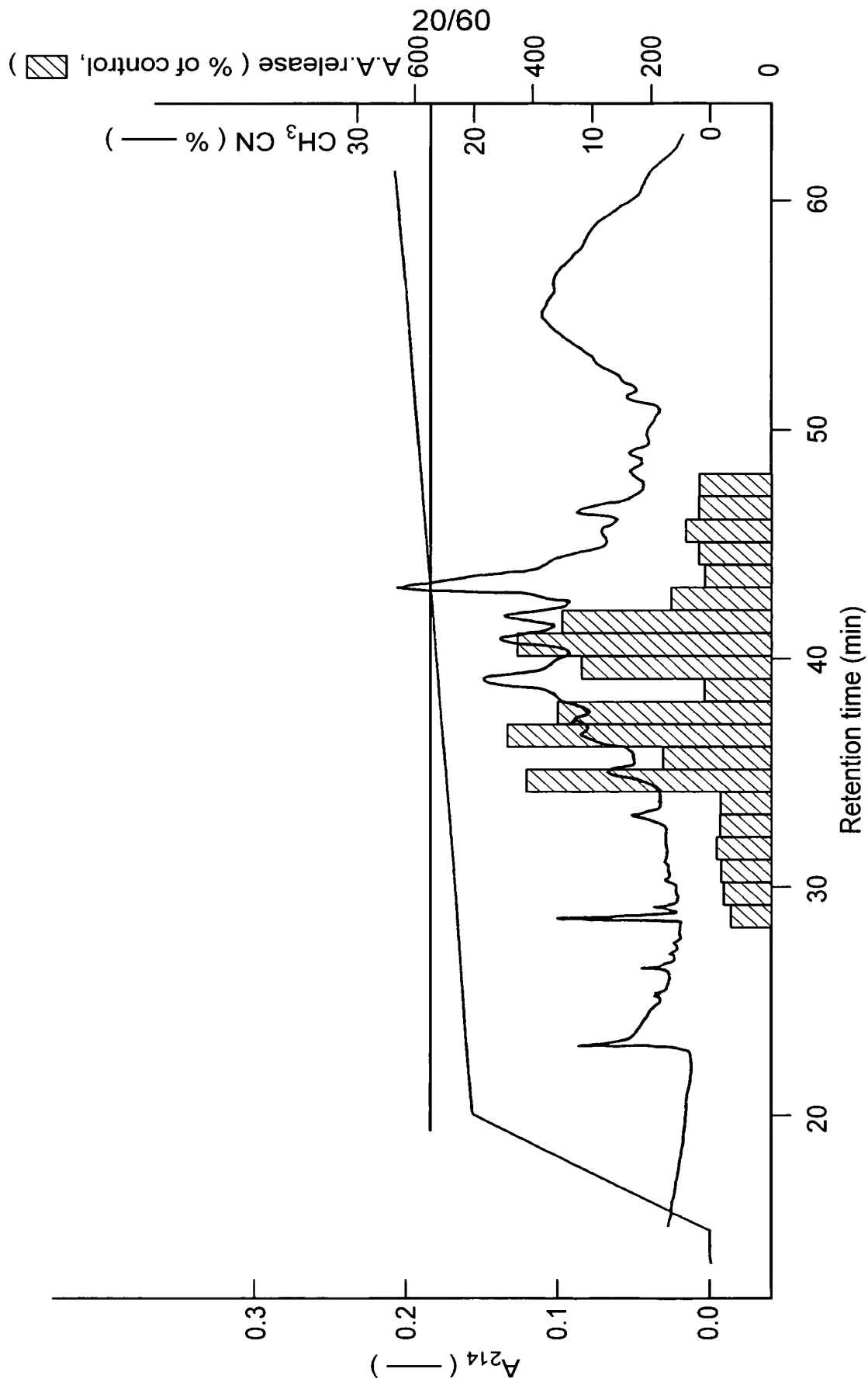


FIG. 18



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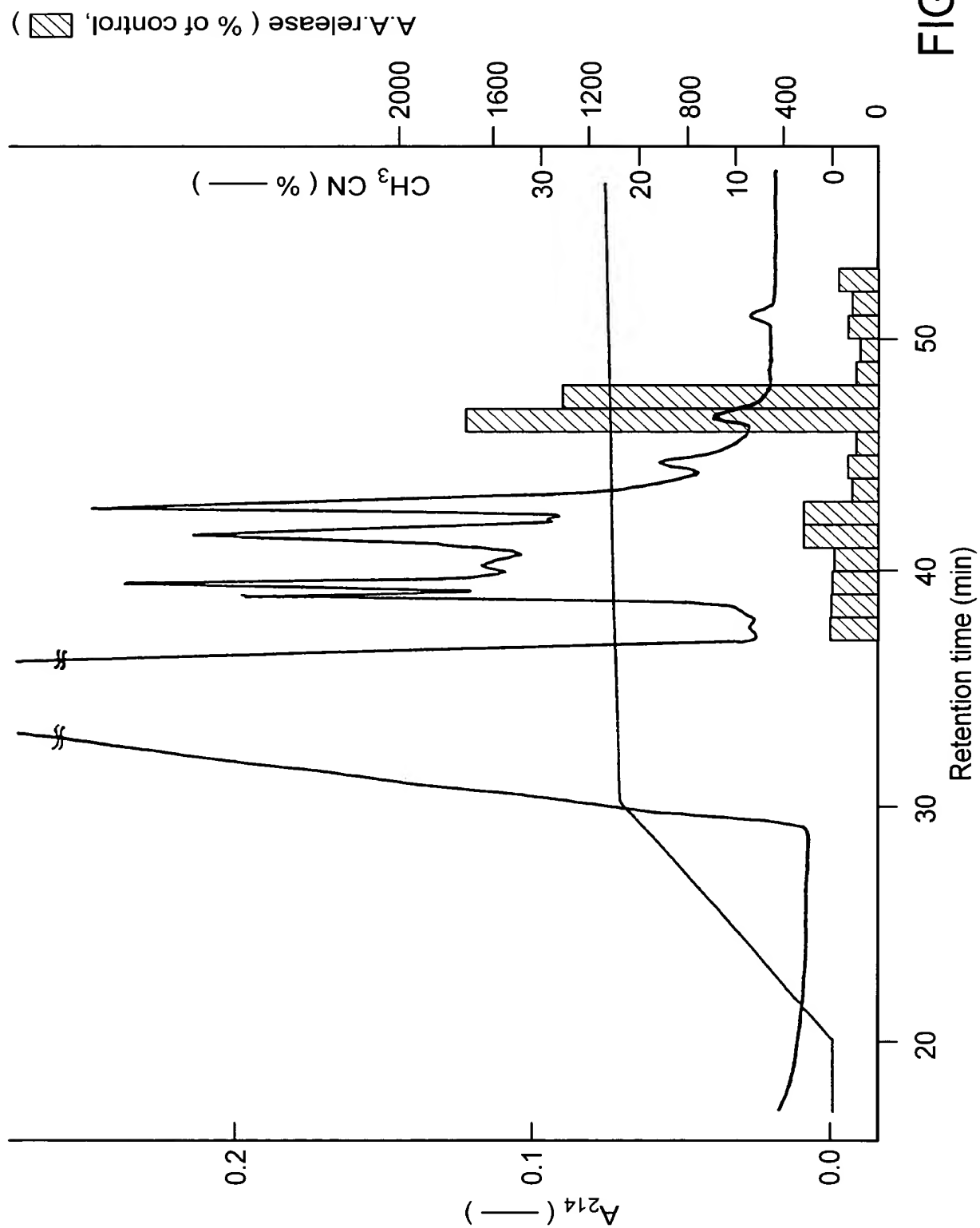
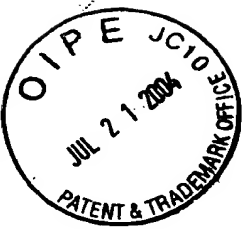
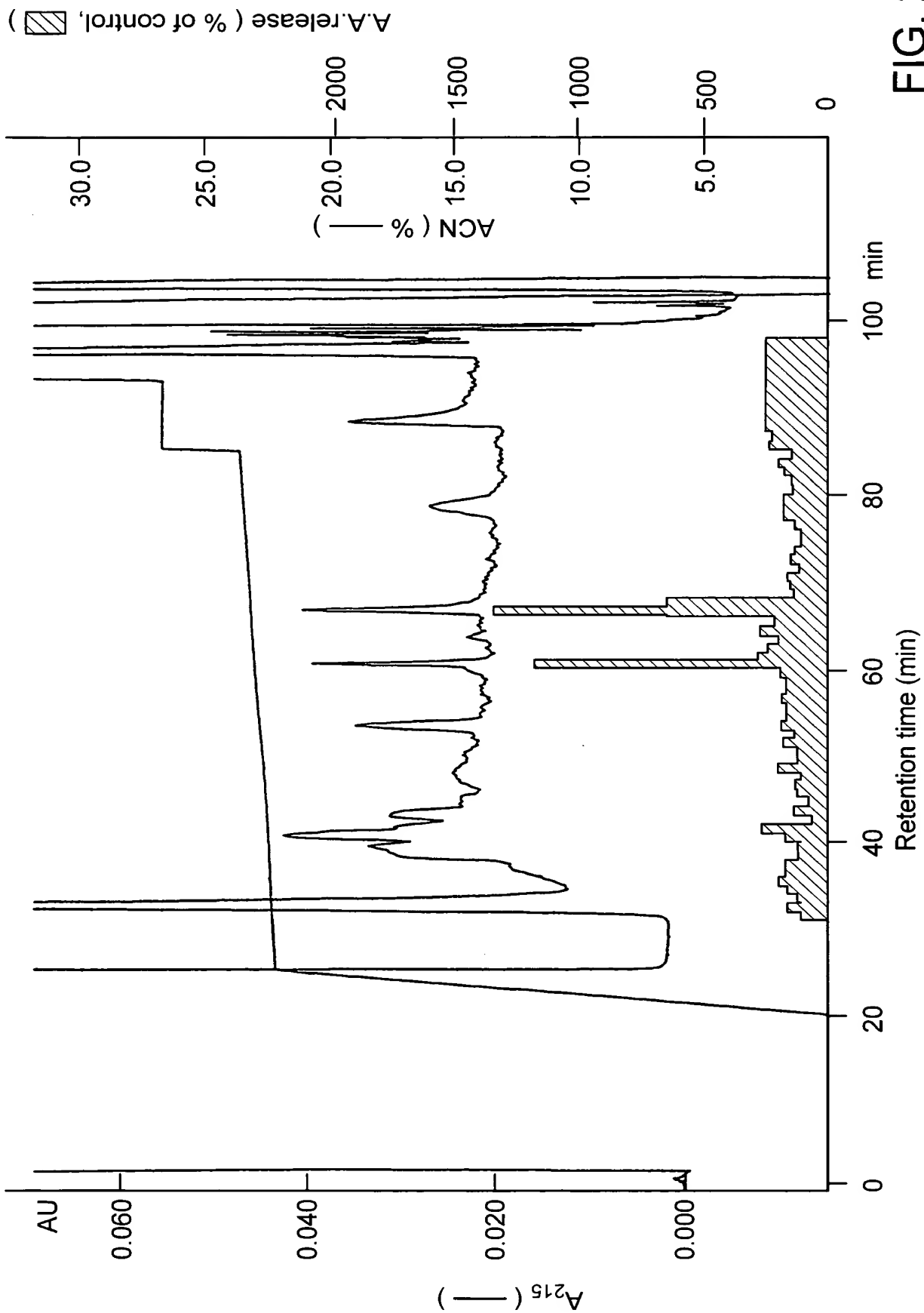


FIG. 19



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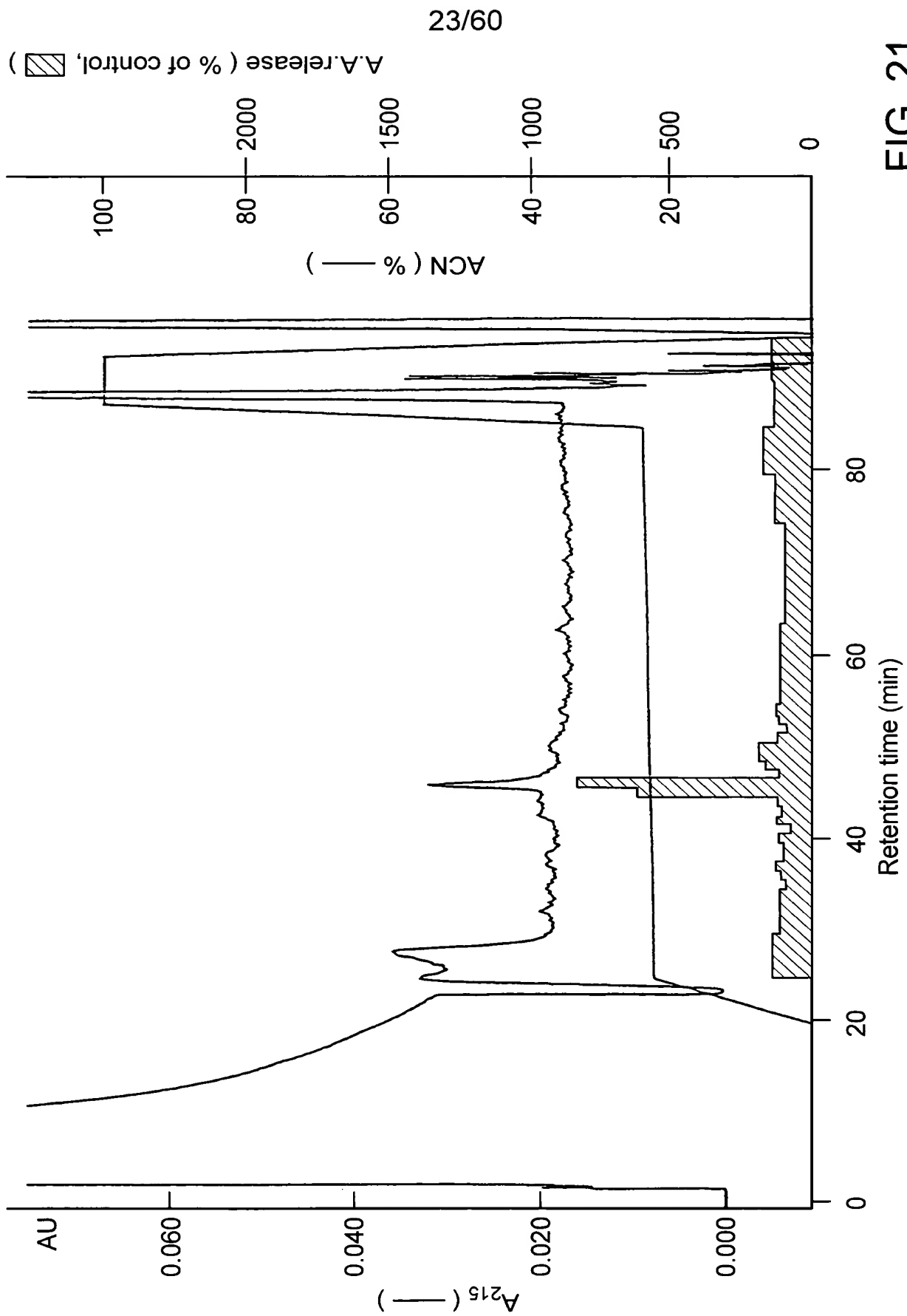
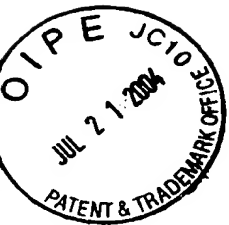


FIG. 21





FIG. 22

P3-2

FIG. 23

1	GTGGAATGAAGCGGTGGGGCGCTGGCTCCTCTGCTGCTGCTGCTGGCCCTGGCCCTG	59
1	MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuGlyLeuAlaLeu	18
60	CAGGGGCTGCCAGCAGAGCCACAGCACTCCATGGAGATCCGCACCCCGACATCAAC	119
19	GlnGlyAlaAlaSerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn	38
120	CCTGCCTGTACGCRGGCCGTGGGATCCGGCCCGTGGCCCGCTTCGGCCGGCGAAGAGCT	179
39	ProAlaTrpTyrAlaGlyArgGlyIleArgProValGlyArgPheGlyArgArgArgAla	58
180	GCCCCGGGGACGGACCCAGGCCCTGGCCCCCGGCGTGTGCCGGCCTGCTTCCGCCCTGGAA	239
59	AlaProGlyAspGlyProArgProGlyProArgValProAlaCysPheArgLeuGlu	78
240	GGCGGYGCTGAGCCCTCCCGAGCCCTCCCGGGGGGCTGACGGCCCGAGCTGGTCCAGGAA	299
79	GlyGlyAlaGluProSerArgAlaLeuProGlyArgLeuThrAlaGlnLeuValGlnGlu	98
300	TAAACAGGGGAGCCTGCCCCCCCCCTCCTCCTCCACCAGCCACCTTCCCCCAGTCCT	359
98		98
360	AATAAAAGCAGCTGGCTTGTT	380
98		98

FIG. 24A

1 GTGGAATGAAGCGGTGGGGCCCTGGCTCCTCTGCTGCTGCTGGCCCTGGCCCTG 59  
1 MetLysAlaValGlyAlaTrpLeuLeuCysLeuLeuLeuGlyLeuAlaLeu 18  
60 CAGGGGGCTGCCAGCAGAGCCCACCAGCACTCCATGGAGATCCGCACCCCCGACATCAAC 119  
19 GlnGlyAlaAlaSerArgAlaHisGlnHisSerMetGluIleArgThrProAspIleAsn 38  
120 CCTGCCTGGTACGCRGGCCGTGGGATCCGGCCCCGTGGGCCTTCGGCCGGCGAAGAGCT 179  
39 ProAlaTrpTyrAlaGlyArgGlyIleArgProValGlyArgPheGlyArgArgAla 58  
180 GCCCTGGGGACGACCCAGGCCCTGGCCCCCGGCGTGTGCCGGCCTGCTTCCGCCCTGGAA 239  
59 AlaLeuGlyAspGlyProArgProGlyProArgValProAlaCysPheArgLeuGlu 78  
240 GCGGYGCTGAGCCCTCCCGAGCCCTCCCGGGGGCTGACGGCCCGAGCTGGTCCAGGAA 299  
79 GlyGlyAlaGluProSerArgAlaLeuProGlyArgLeuThrAlaGlnLeuValGlnGlu 98  
300 TAACAGCGGAGCCTGCCCCCACCCTCCTCCTCCACCAGCCACCTTCCCCCAGTCCT 359  
98 98  
360 AATAAAGCAGCTGGCTTGTT 380  
98 98

FIG. 24B

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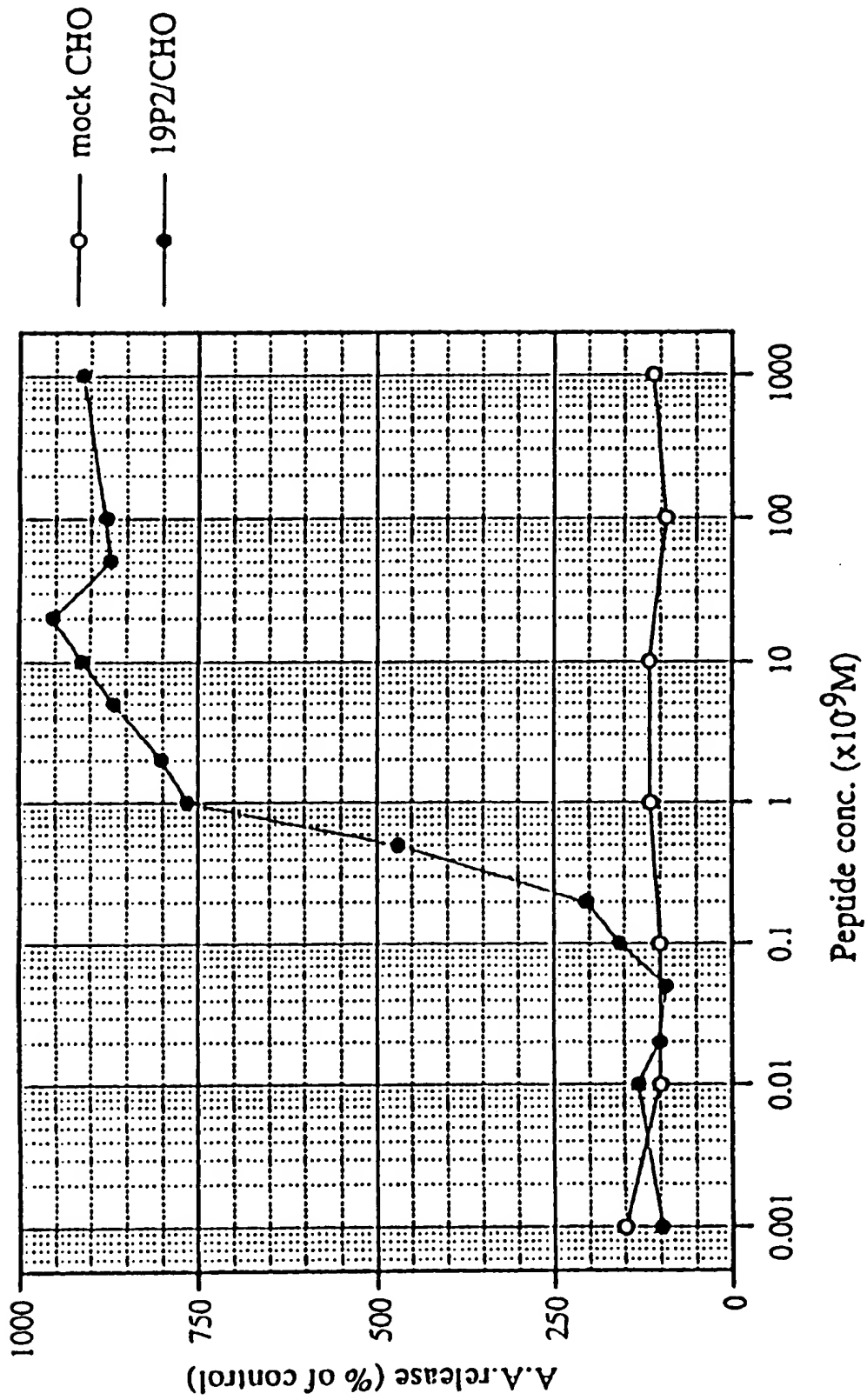


FIG. 25

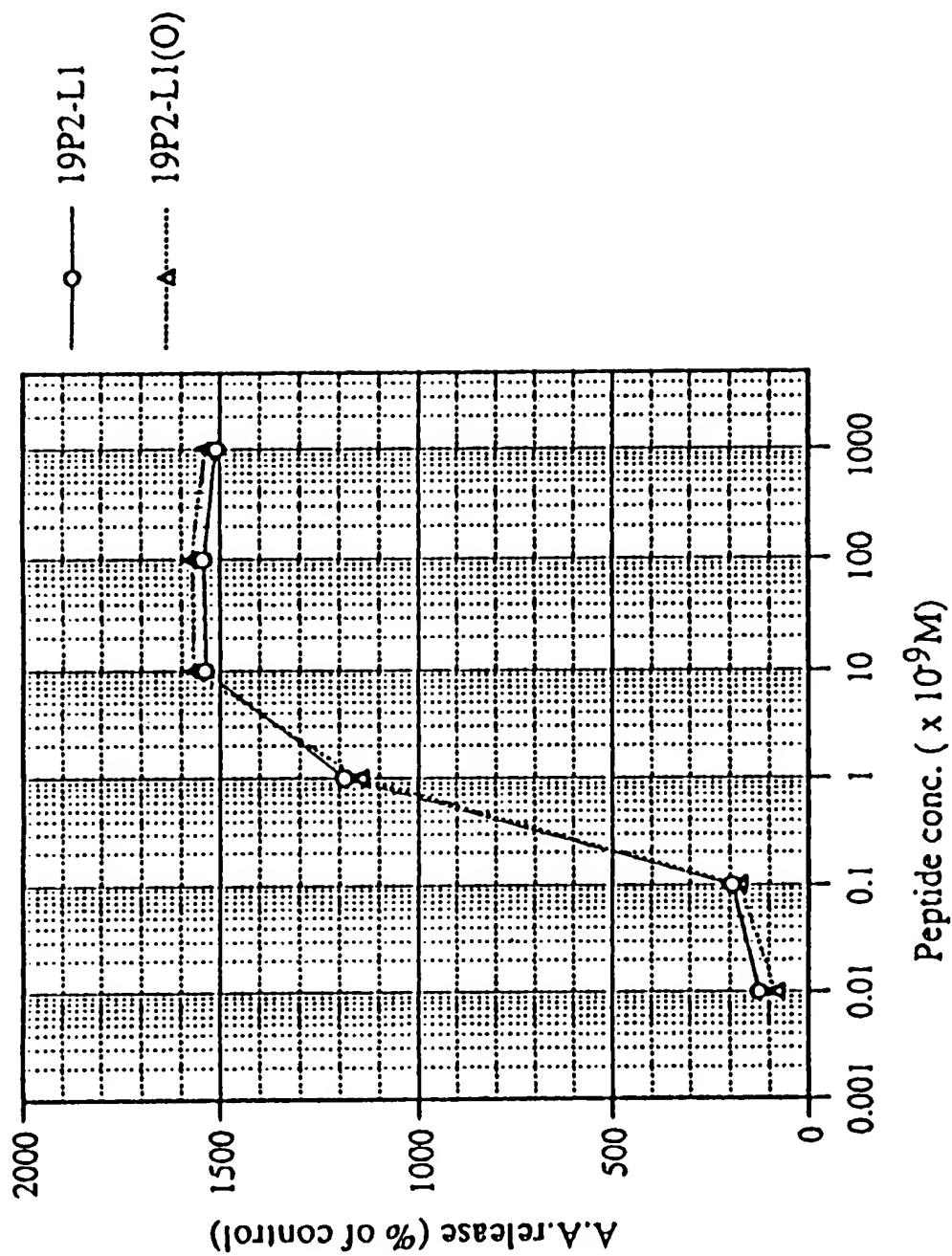


FIG. 26

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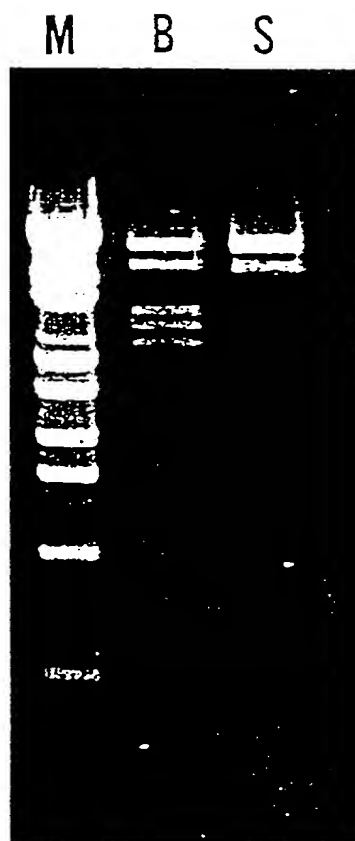
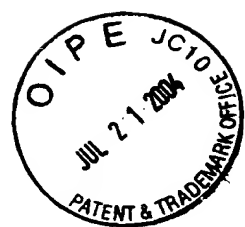


FIG. 28



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10	20	30	40	50	60
ATGAAGGCGG	TGGGGGCCTG	GCTCCTCTGC	CTGCTGCTGC	TGGGCCTGGC	CCTGCAGGGG
70	80	90	100	110	120
GCTGCCAGCA	GAGCCACCA	GCACTCCATG	GAGATCCGCA	GTGAGTGTCT	AGCCCCGCCC
130	140	150	160	170	180
CTGCCCCCAG	GGGTCACAGG	GGGGGCCTGG	CCACTTCCTG	GGCTGGGACA	TCCTTGCTAA
190	200	210	220	230	240
GCATCCTGGG	GTGGGGTTT	GGCCTCCTGT	TCCCCAGACC	CTTCCCCCAG	GTGGCCCCGA
250	260	270	280	290	300
CAGGTGCTCC	CAAGGGTCCC	GGCCCAGCAC	ACGGGGGAGG	GTCACTCCTC	ACCACACGGG
310	320	330	340	350	360
TGGCCTGGGG	CTGAGTGCAC	GTCACCCATG	AGAACGGGGC	TGTGAGGACA	GGAAAGGAAG
370	380	390	400	410	420
GGGAGTGTGT	CCTGGTGTGA	GTCTGAAATC	CTACTTCCCA	AAGCCACCCC	AGCACCAGAA
430	440	450	460	470	480
ATGGGCGCTC	CGGGTGAACC	TCCTGTGCGG	GTGGGTGGTC	CTGGCATGGC	CTGGGCGACA
490	500	510	520	530	540
GGCAGCCATG	AGCTGAGCAC	ACACCCGGCC	CGGCCACCAG	GGCTGTATGC	TCCAGGGCAC
550	560	570	580	590	600
AGGCCTCCAT	GCGCTCTTCT	CTCTCTTTCC	AGCCCCCGAC	ATCAACCCTG	CCTGGTACGC
610	620	630	640	650	660
AGGCCGTGGG	ATCCGGCCCG	TGGGCCGCTT	CGGCCGGCGA	AGAGCTGCCC	TGGGGGACGG
670	680	690	700	710	720
ACCCAGGCCT	GGCCCCCGGC	GTGTGCCGGC	CTGCTTCCGC	CTGGAAGGCG	GTGCTGAGCC
730	740	750	760	770	780
CTCCCGAGCC	CTCCCGGGGC	GGCTGACGGC	CCAGCTGGTC	CAGGAATAA.	.....

FIG. 29



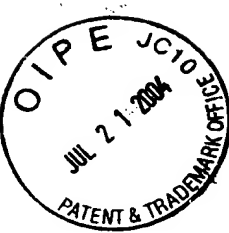


FIG. 30A
FIG. 30B
FIG. 30C

FIG. 30

genome	1	ATGAAGCGG	10	TGGGGCCTG	20	GCTCCTCTGC	30	CTGCTGCTGC	40	TGGGCCTGGC	50
cDNA	1	ATGAAGCGG	10	TGGGGCCTG	20	GCTCCTCTGC	30	CTGCTGCTGC	40	TGGGCCTGGC	50
genome	51	CCTGCAGGG	60	GCTGCCAGCA	70	GAGCCACCA	80	GCACTCCATG	90	GAGATCCGCA	100
cDNA	51	CCTGCAGGG	60	GCTGCCAGCA	70	GAGCCACCA	80	GCACTCCATG	90	GAGATCCGCA	100
genome	101	GTGAGTGTCT	110	AGCCCCGCC	120	CTGCCCCCAG	130	GGTCACAGG	140	GGGGCCTGG	150
cDNA	101	GTGAGTGTCT	110	AGCCCCGCC	120	CTGCCCCCAG	130	GGTCACAGG	140	GGGGCCTGG	150
genome	151	CCACTTCCTG	160	GGCTGGGACA	170	TCCTTGCTAA	180	GCACTCCTGG	190	GTGGGGTTT	200
cDNA	151	CCACTTCCTG	160	GGCTGGGACA	170	TCCTTGCTAA	180	GCACTCCTGG	190	GTGGGGTTT	200

FIG. 30A

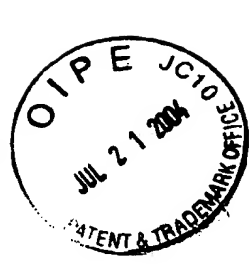
genome	201	210	220	230	240	250
cDNA	201	210	220	230	240	250
	GGCCTCCTGT	TCCCCAGACC	CTTCCCCCAG	GTGGCCCGGA	CAGGTGCTCC	
	-----	-----	-----	-----	-----	
genome	251	260	270	280	290	300
cDNA	251	260	270	280	290	300
	CAAGGTCCC	GGCCCAGCAC	ACGGGGGAGG	GTCACCTCCTC	ACCACACGGG	
	-----	-----	-----	-----	-----	
genome	301	310	320	330	340	350
cDNA	301	310	320	330	340	350
	TGGCCTGGG	CTGAGTGCAC	GTCACCCATG	AGAACGGGGC	TGTGAGGACA	
	-----	-----	-----	-----	-----	
genome	351	360	370	380	390	400
cDNA	351	360	370	380	390	400
	GGAAAGGAAG	GGGAGTGTGT	CCTGGTGTGA	GTCTGAATC	CTACTTCCCA	
	-----	-----	-----	-----	-----	
genome	401	410	420	430	440	450
cDNA	401	410	420	430	440	450
	AAGCCACCCC	AGCACCAGAA	ATGGGGCGTC	CGGGTGAACC	TCCTGTGCGG	
	-----	-----	-----	-----	-----	
genome	451	460	470	480	490	500
cDNA	451	460	470	480	490	500
	GTGGGTGGTC	CTGGCATGGC	CTGGGGGACA	GGCAGCCATG	AGCTGAGCAC	
	-----	-----	-----	-----	-----	

FIG. 30B



genome	510	520	530	540	550
cDNA	501 ACACCCGGCC	CGGCCACCAG	GGCTGTATGC	TCCAGGGCAC	AGGCCTCCAT
	551 -----	520 -----	530 -----	540 -----	550 -----
genome	560	570	580	590	600
cDNA	551 GCGCTCTTCT	CTCTCTTTCC	AGCCCCCGAC	ATCAACCCCTG	CCTGGTACGC
	551 -----	570 -----	580 -----	590 -----	600 -----
genome	610	620	630	640	650
cDNA	601 AGGCCGTGGG	ATCCGGCCCCG	TGGCCCGCTT	CGGCCGGCGA	AGAGCTGCCC
	601 GGGCCGTGGG	ATCCGGCCCCG	TGGCCCGCTT	CGGCCGGCGA	AGAGCTGCCC
genome	660	670	680	690	700
cDNA	651 TGGGGACGG	ACCCAGGCCT	GGCCCCCGGC	GTGTGCCGGC	CTGCTTCCGC
	651 CGGGGACGG	ACCCAGGCCT	GGCCCCCGGC	GTGTGCCGGC	CTGCTTCCGC
genome	710	720	730	740	750
cDNA	701 CTGGAAGCG	GTGCTGAGCC	CTCCCGAGCC	CTCCCGGGGC	GGCTGACGGC
	701 CTGGAAGCG	GGCTGAGCC	CTCCCGAGCC	CTCCCGGGGC	GGCTGACGGC
genome	760	770	780	790	800
cDNA	751 CCAGCTGGTC	CAGGAATAA.	.....	.....	.....
	751 CCAGCTGGTC	CAGGAATAA.	.....	.....	.....

FIG. 30C



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5'	9	18	27	36	45	54
ATG AAG GCG GTG GGG GCC TGG CTC CTC TGC CTG CTG GGC CTG GCC CTG						
M K A V G A W L L C L L L G L A L						
63	72	81	90	99	108	
CAG GGG GCT GCC AGC AGA GCC CAC CAG CAC TCC ATG GAG ATC CGC ACC CCC GAC						
Q G A A S R A H Q H S M E I R T P D						
117	126	135	144	153	162	
ATC AAC CCT GCC TGG TAC GCA GGC CGT GGC ATC CGG CCC GTG GGC CGC TTC GGC						
I N P A W Y A G R G I R P V G R F G						
171	180	189	198	207	216	
CGG CGA AGA GCT GCC CTG GCG GAC GGA CCC AGG CCT GGC CCC CGC CGT GTG CCG						
R R R A A L G D G P R P G P R R V P						
225	234	243	252	261	270	
GCC TGC TTC CGC CTG GAA GGC GGT GCT GCT GAG CCC TCC CGA GCC CTC CCG GGG CCG						
A C F R L E G G A E P S R A L P G R						
279	288	297				
CTG ACG GCC CAG CTG GTC CAG GAA TAA 3'						
L T A Q L V Q E *						

FIG. 31

1 GGCAATCATCCAGGAAGACGGAGCATGGCCCTGAAGACGTGGCTTCTGTGCTTGCTGCTG 59  
1 MetAlaLeuLysThrTrpLeuLeuCysLeuLeuLeu 12  
1  
60 CTAAGCTTGGTCCCTCCAGGGGCTTCAGCCGAGCCACCAGCACTCCATGGAGACAAGA 119  
13 LeuSerLeuValLeuProGlyAlaSerSerArgAlaHisGlnHisSerMetGluThrArg 32  
120 ACCCCTGATATCAATCCTGCCTGGTACACGGGCCCGGGATCAGGCCCTGTGGCCGCTTC 179  
33 ThrProAspIleAsnProAlaTrpTyrThrGlyArgGlyIleArgProValGlyArgPhe 52  
180 GGCAGGAGAAGGCAACCCGAGGGATGTCACTGGACTTGGCCAACTCAGCTGCCTCCCA 239  
53 GlyArgArgArgAlaThrProArgAspValThrGlyLeuGlyGlnLeuSerCysLeuPro 72  
240 CTGGATGGACGCACCAAGTTCTCTCAGCGTGGATAACACCCAGCTCGAGAAGACAGTGC 299  
73 LeuAspGlyArgThrLysPheSerGlnArgGly\*\*\* 83  
300 TGCTGAGCCCAAGCCCACTCCCTGTCCCTGCAGACCCCTCCTCTACCCCTCCCTCTCCT 359  
83 83  
360 CTGCT 364  
83 83

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FIG. 32

FIG. 33A
FIG. 33B

bovine.aa

bovine.seq -18 .....GT GGAATGAAGG CCGTGGGGGC CTGGCTCCTC 32  
rat.seq 1 GGCAATCATCC AGGAAGACGG AGCATG---G CCTGAAGAC GTGGCTTCTG 50

bovine.aa

C L L L L G L A L Q G A A S R A H  
60 70 80 90 100

bovine.seq

33 TGCCTGCTGC TGCTGGGCTT GGCCCTGCAG GGGGCTGCCA GCAGAGCCCA 82  
51 TGCTTGCTGC TGCTAAGCTT GGTCTCTCCA GGGGCTTCCA GCGAGCCCA 100

bovine.aa

Q H S M E I R T P D I N P A W Y A  
110 120 130 140 150

bovine.seq

83 CCAGCACTCC ATGGAGATCC GCACCCCGCA CATCAACCCT GCCTGGTACG 132  
101 CCAGCACTCC ATGGAGACAA GAACCCCTGA TATCAATCCT GCCTGGTACA 150

bovine.aa

G R G I R P V G R F G R R R A A  
160 170 180 190 200

bovine.seq

133 CGGGCCGTGG GATCCGGCCC GTGGCCGCTT TCGGCCGGG AAGAGCTGCC 182  
151 CGGGCCGGG GATCAGGCCT GTGGCCGCTT TCGGCAGGAG AAGGCAACC 200

rat.seq

151 CGGGCCGGG GATCAGGCCT GTGGCCGCTT TCGGCAGGAG AAGGCAACC 200

FIG. 33

FIG. 33A

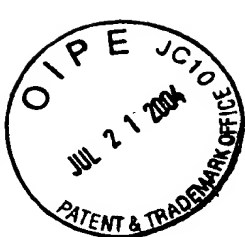
bovine.aa	P G D G P R P G P R R V P A C F R	
	210 220 230 240 250	
bovine.seq	183 CCGGGGACG GACCCAGGC TGGCCCCCGG CGTGTCGGG CCTGCTMCCG	232
rat.seq	201 CCGAGGGATG TCACTGGACT TGGC-----CAACTCA GCTGCCCTGCC	250
bovine.aa	L E G G A E P S R A L P G R L T A	
	260 270 280 290 300	
bovine.seq	233 CCTGGAAGGC GGCCTGAGC CTTCCCGAGC CTTCCCGGG CCGCTGACGG	282
rat.seq	251 ACTGGATGGA CGACCAAGT TCTCTCAGCG TGGATAACAC CCCAGCTCGA	300
bovine.aa	Q L V Q E *	
	310 320 330 340 350	
bovine.seq	283 CCCAGCTGGT CCAGGAATAA CAGCGGAGC CTGCCCCCCA CCCCCTCTCC	332
rat.seq	301 GAAGACAGTG CTGCTGAGCC CAAGCCCACA CTCCCTGTCC CCTGCAGACC	350
	360 370 380 390 400	
bovine.seq	333 TCCACCAGCC ACCTTCCCTC CAGTCCTAAT AAAAGCAGCT GGCTTGT...	382
rat.seq	351 CTCCTCTACC CTCCTCTCC TCIGCT.....	400

FIG. 33B

1 GGCCTCCTCGGAGGAGCC AAGGATGAAGTGCTGAGGGCCTGGCTCCTGTGCCTGCTG 59  
12 MetLysValLeuArgAlaTrpLeuLeuCysLeuLeu  
60 ATGCTGGGCTGGCCCTGCGGGAGCTGCAAGTCGTACCCATCGGCACCTCCATGGAGATC 119  
32 MetLeuGlyLeuAlaLeuArgGlyAlaAlaSerArgThrHisArgHisSerMetGluIle  
120 CGCACCCCTGACATCAATCCTGCCTGGTACGCCAGTCGCGGGATCAGGCCCTGTGGGCCCGC 179  
52 ArgThrProAspIleAsnProAlaTrpTyrAlaSerArgGlyIleArgProValGlyArg  
239 TTCGGTCGGAGGAGGCAACCCCTGGGGGACGTCCCCAAGCCTGGCCTGCCACCCCGGCTG 239  
72 PheGlyArgArgAlaThrLeuGlyAspValProLysProGlyLeuArgProArgLeu  
299 ACCTGCTTCCCCCTGGAAGCGGTGCTATGTCGTCCCAGGATGGCTGACAGCCAGCCTTGT 299  
87 ThrCysPheProLeuGluGlyGlyAlaMetSerSerGlnAspGly\*\*\*  
300 CAAGAAACTCACTCTGGAGCCTCCCCCACCCTCTCCTCTCCTCTCGGGCTCCTTTC 359  
87  
360 CC 361  
87

FIG. 34



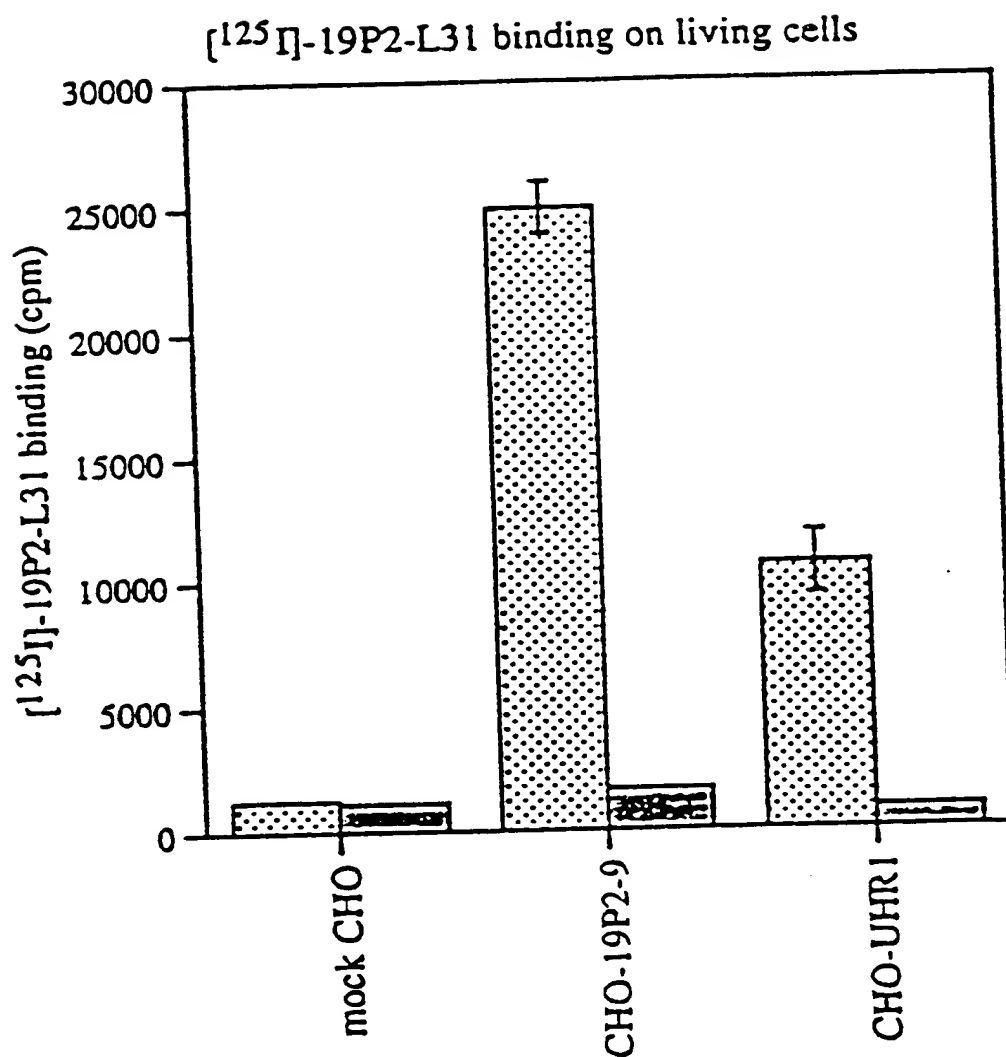


	10	20	30	40	50	
bovine.aa	1 MKAVGAWLLC	LLLLGLALQG	AASRAHQHSM	EIRTPDINPA	WYAGRGIRFV	50
rat.aa	1 M-ALKTWLLC	LLLLSLVLPG	ASSRAHQHSM	ETRTPDINPA	WYTGIRFV	50
human.aa	1 MKVLRWLLC	LLMLGLALRG	AASRTHRHSM	EIRTPDINPA	WYASRGIRFV	50
	60	70	80	90	100	
bovine.aa	51 GRFGRRRAAP	GDGFRFGPRR	VPACFRLEGG	AEPSRALPCR	LTAQLVQE*	100
rat.aa	51 GRFGRRRATP	RDVTGLG---	QLSCLPLDGR	TKFSQRG*	.....	100
human.aa	51 GRFGRRRATL	GDVFKRGLRP	RLTCEPLEGG	AMSSQDG*	.....	100

FIG. 35

▨ Total binding

▨ NSB



cells;  $0.5 \times 10^7$  cells/ml

[<sup>125</sup>I]-19P2-L31; 200pM (avg. 63857.3cpm)

NSB; 200nM (x 1,000)

reaction; RT, 2.5hr

in HBSS + 0.05% BSA + 0.05% CHAPS

in 100  $\mu$ l

FIG. 36

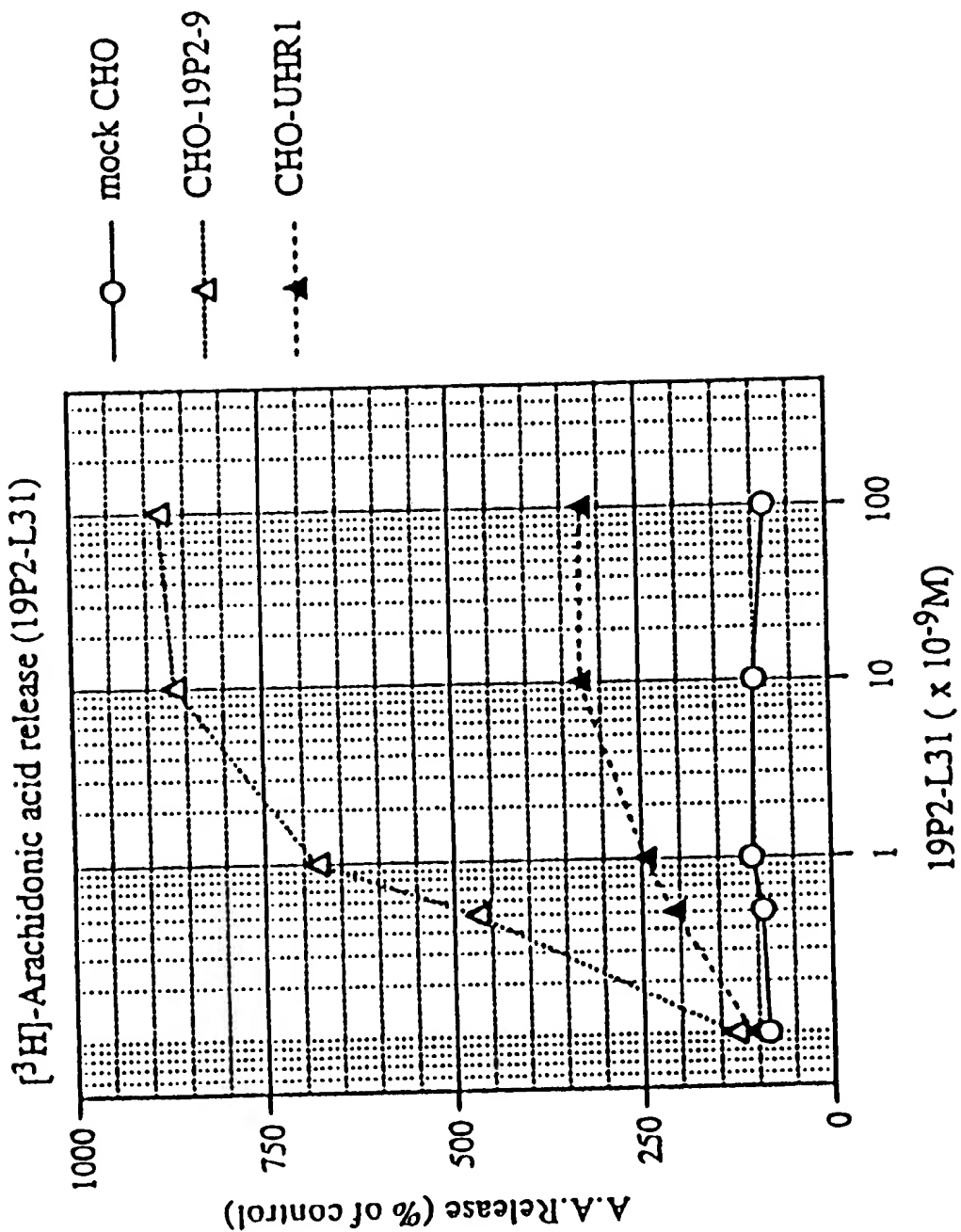


FIG. 37

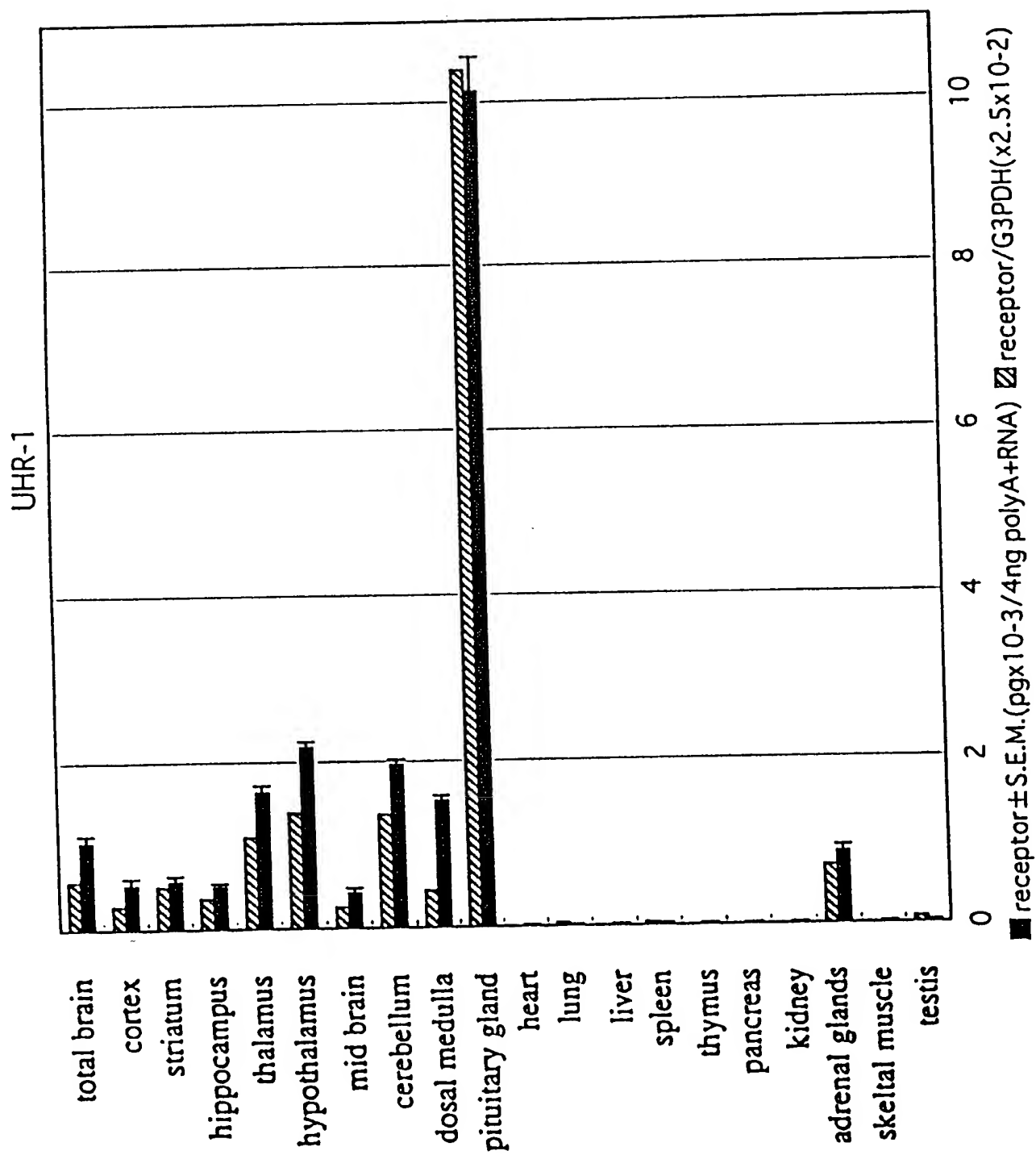


FIG. 38

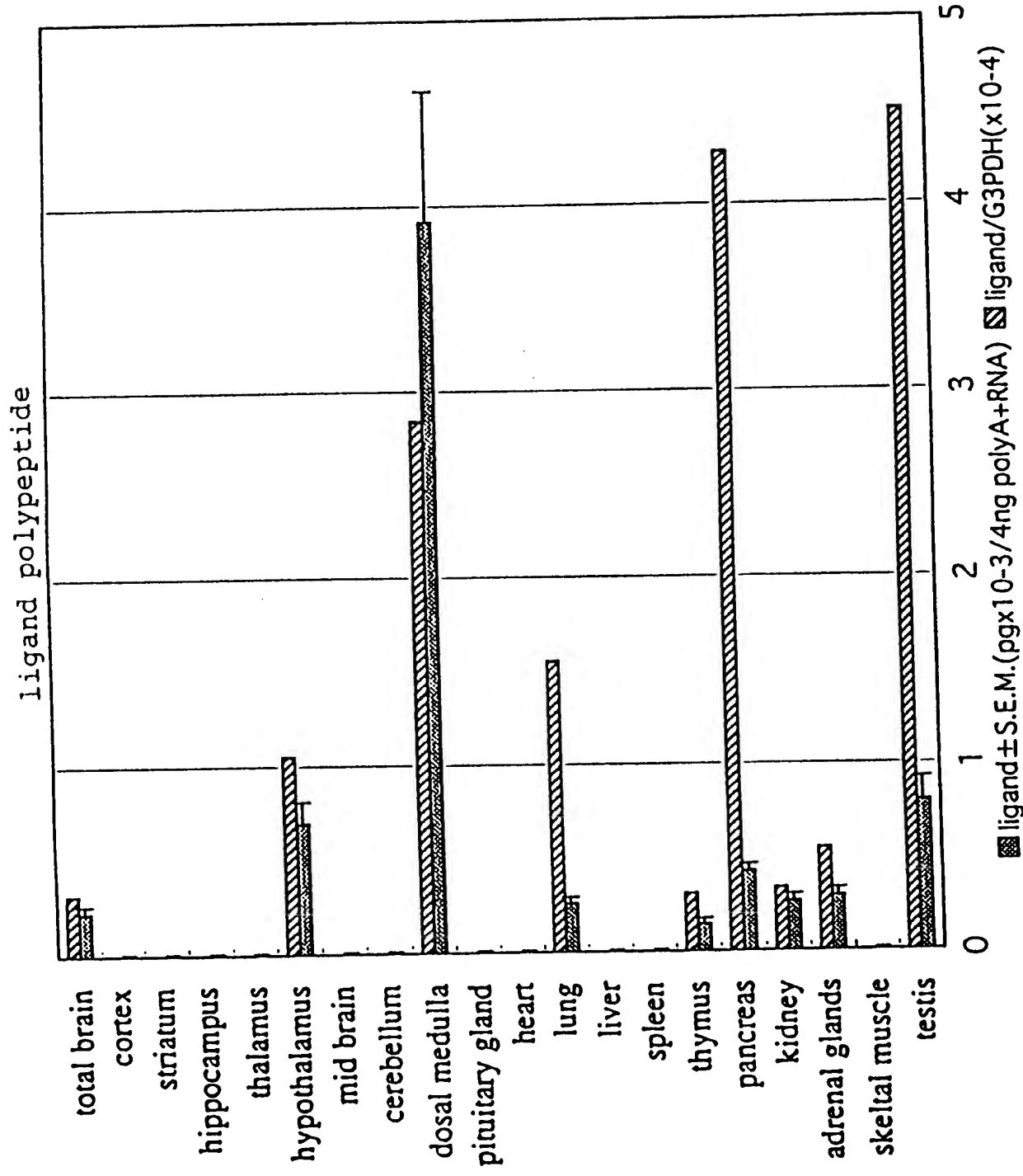


FIG. 39

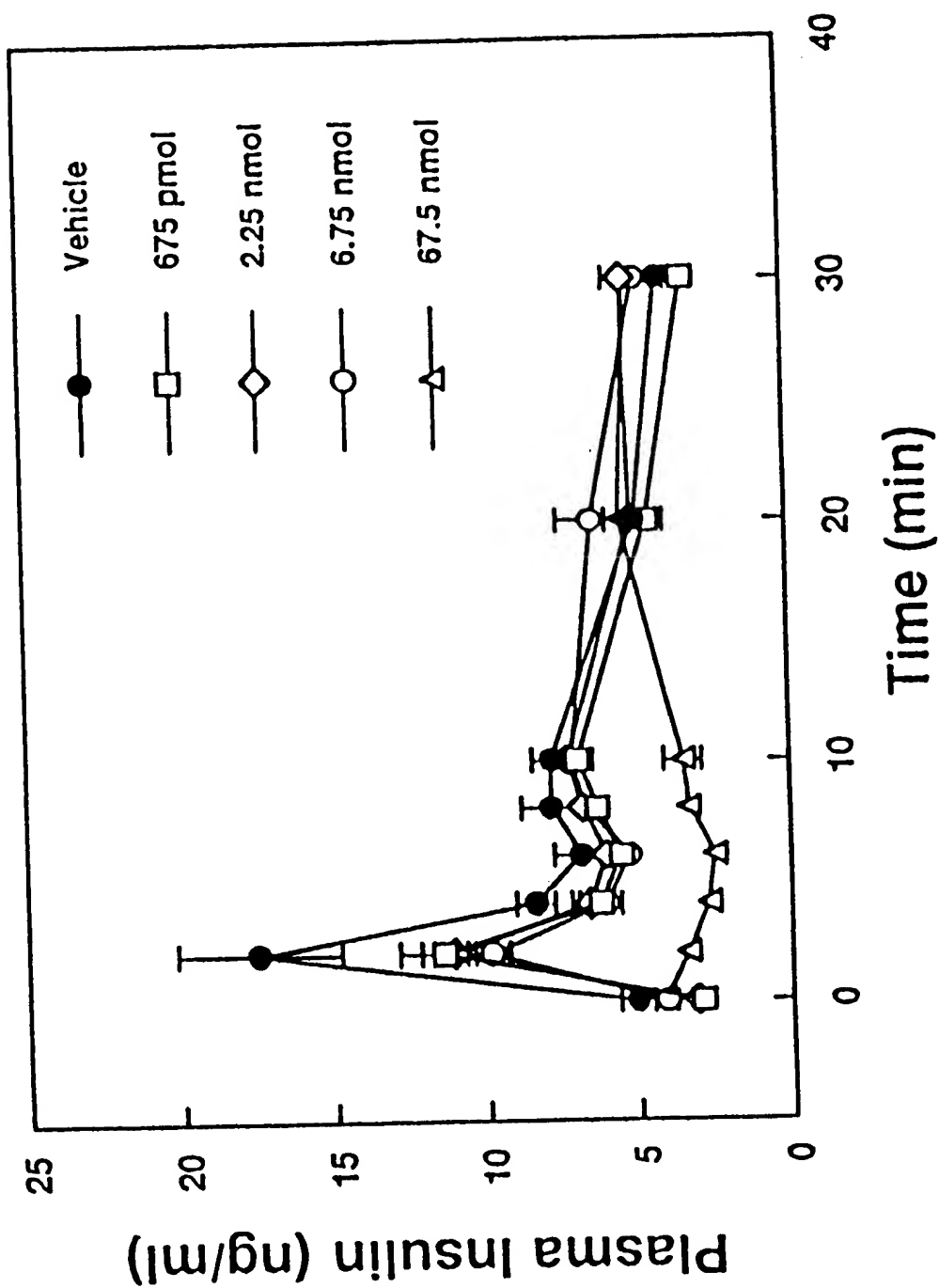


FIG. 40

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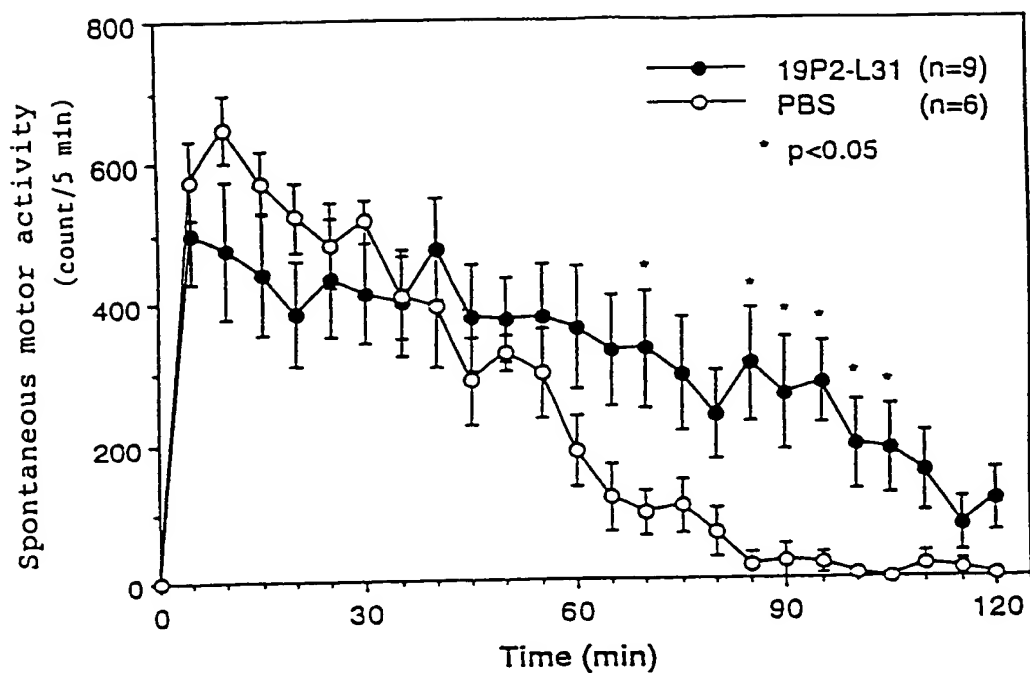


FIG. 41A

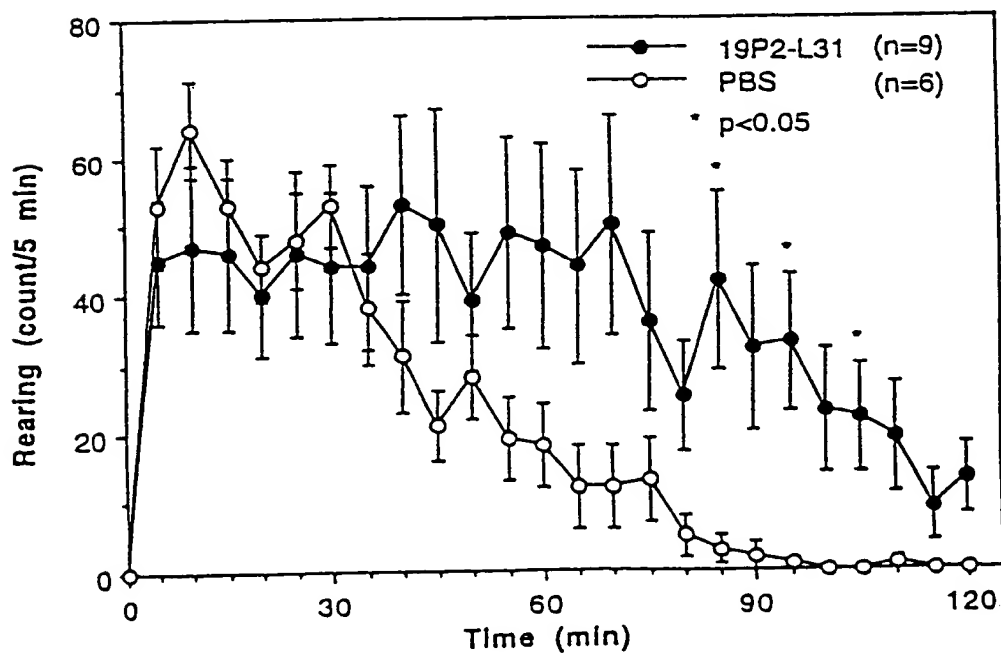


FIG. 41B

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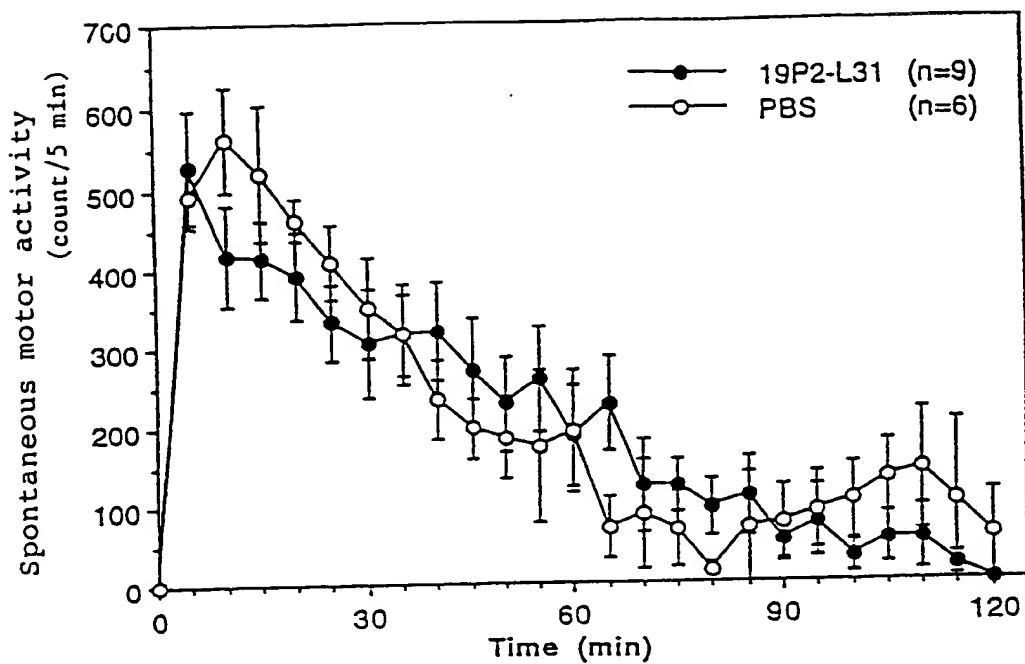


FIG. 42A

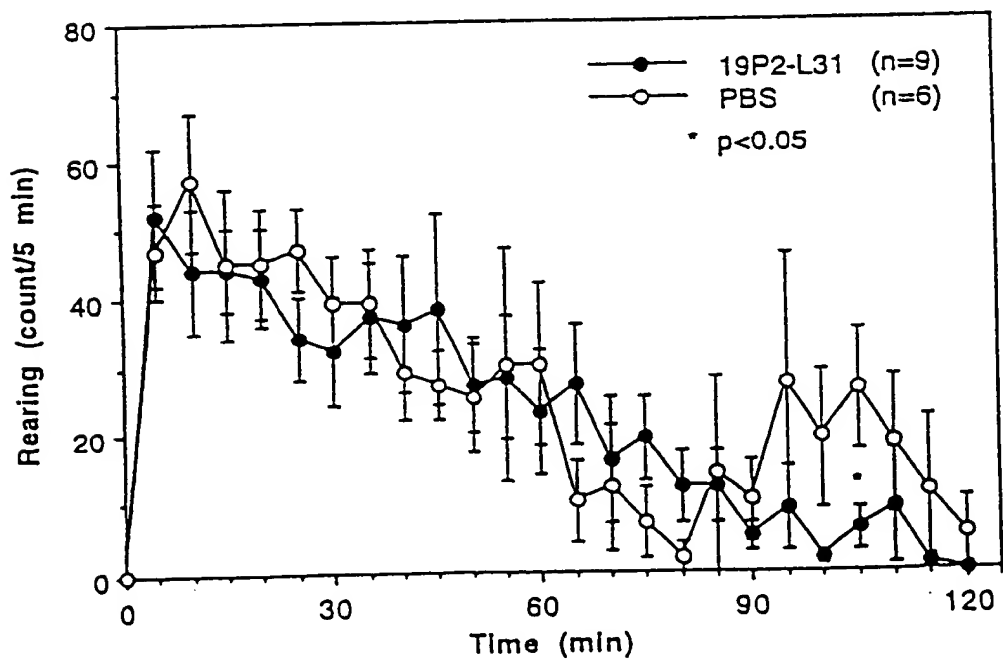


FIG. 42B



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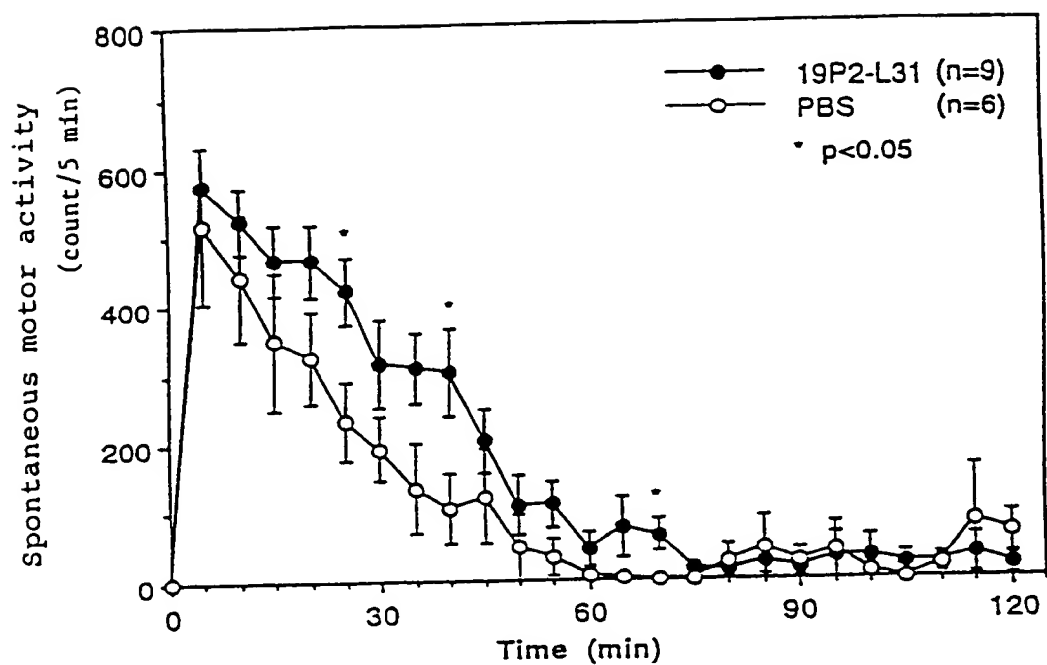


FIG. 43A

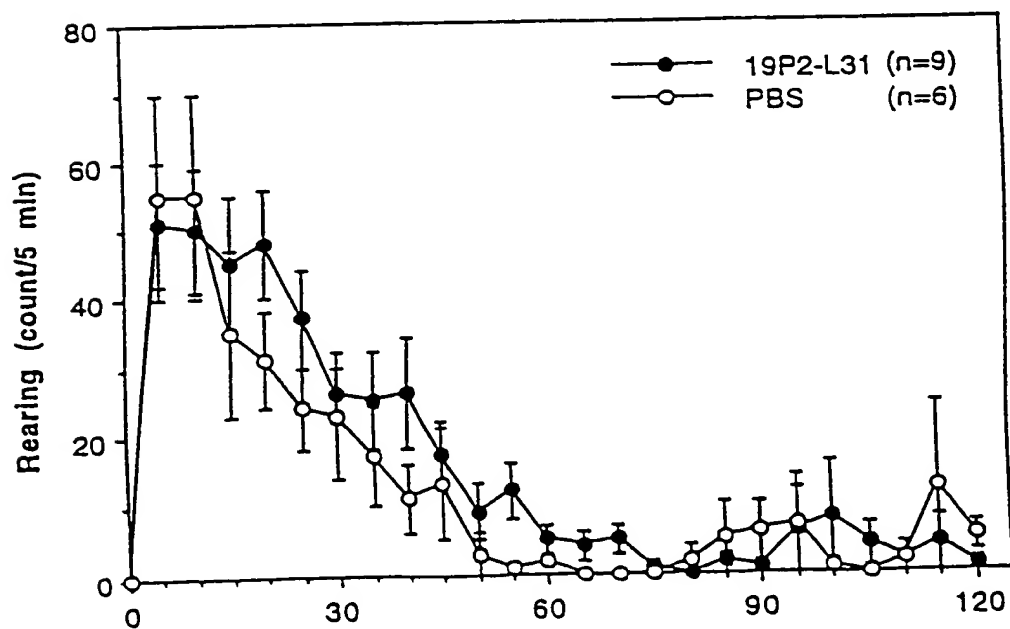


FIG. 43B

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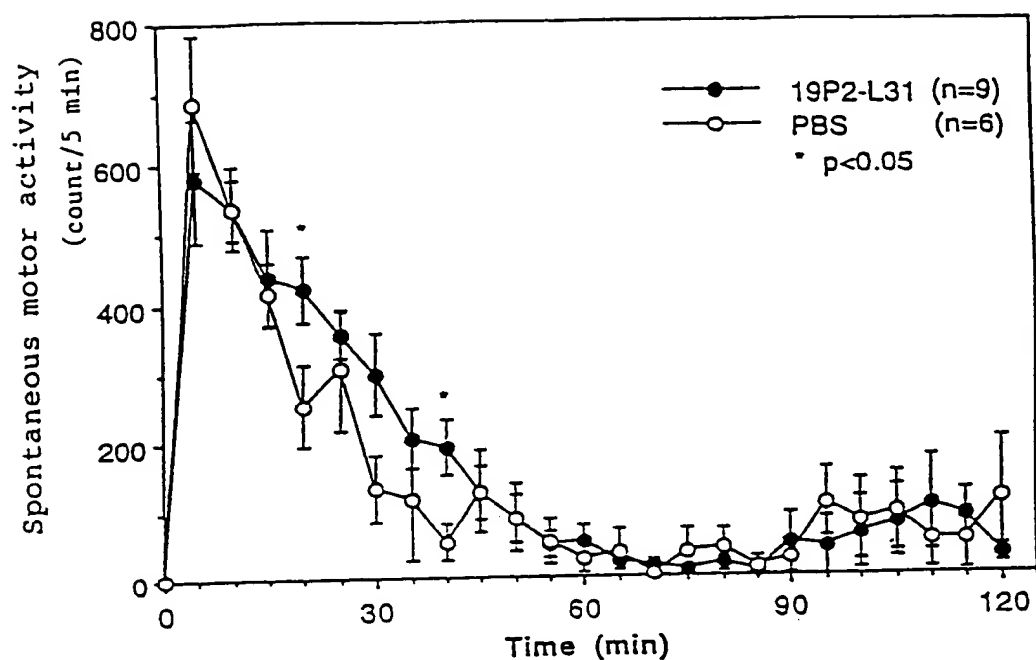


FIG. 44A

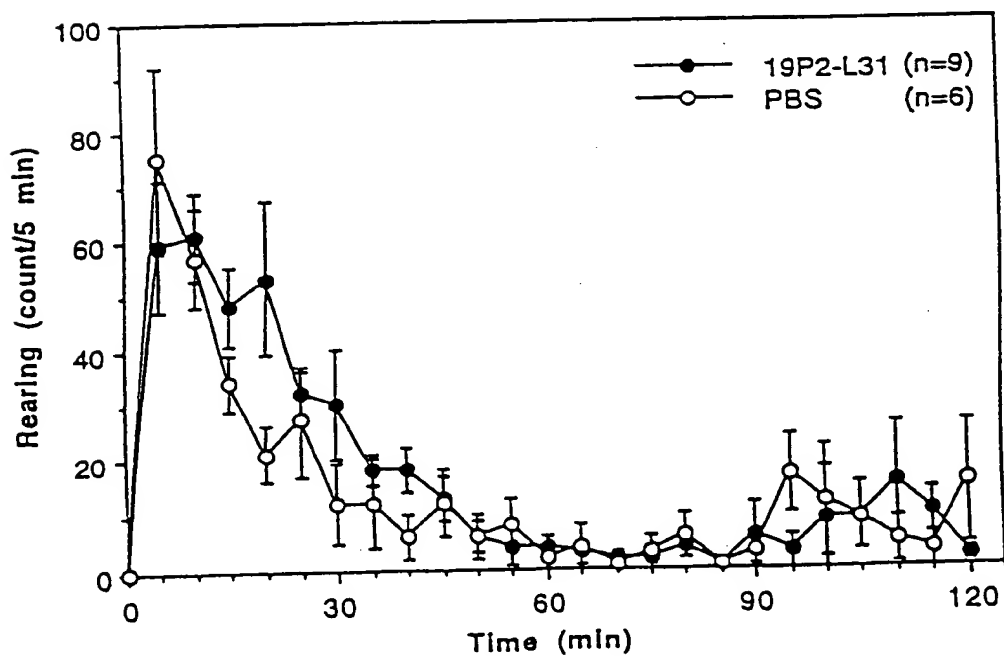


FIG. 44B

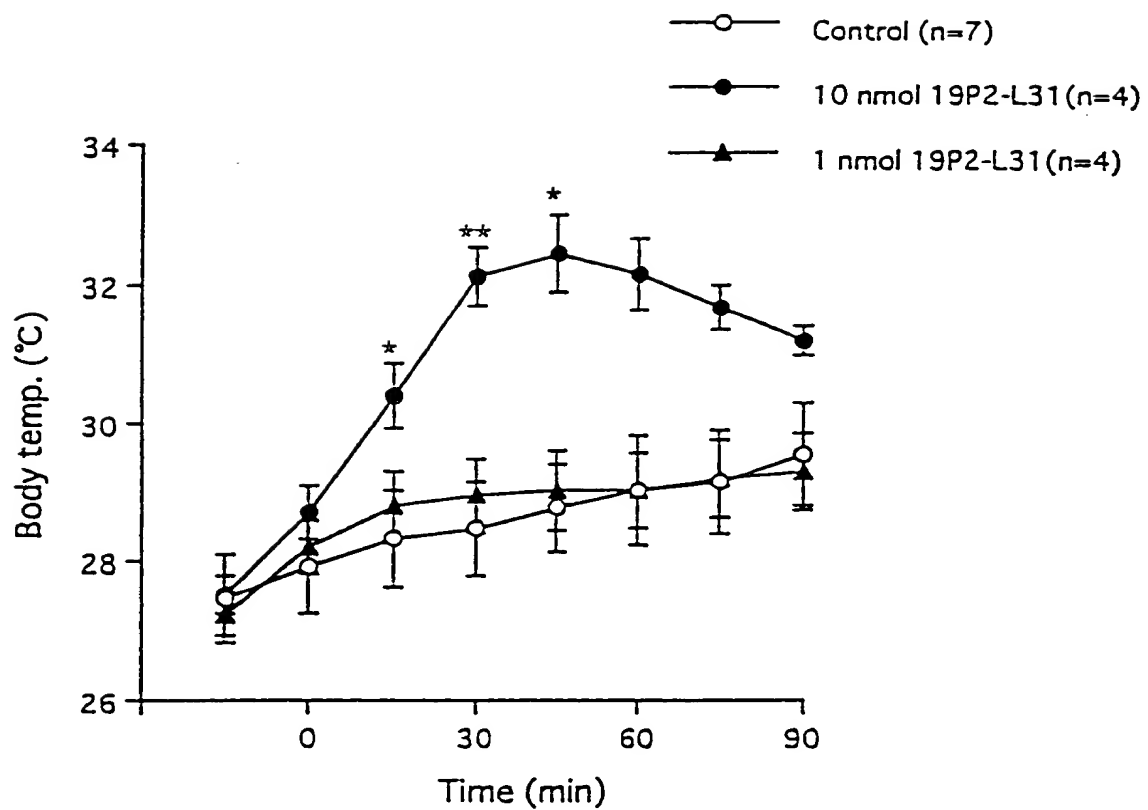


FIG. 45

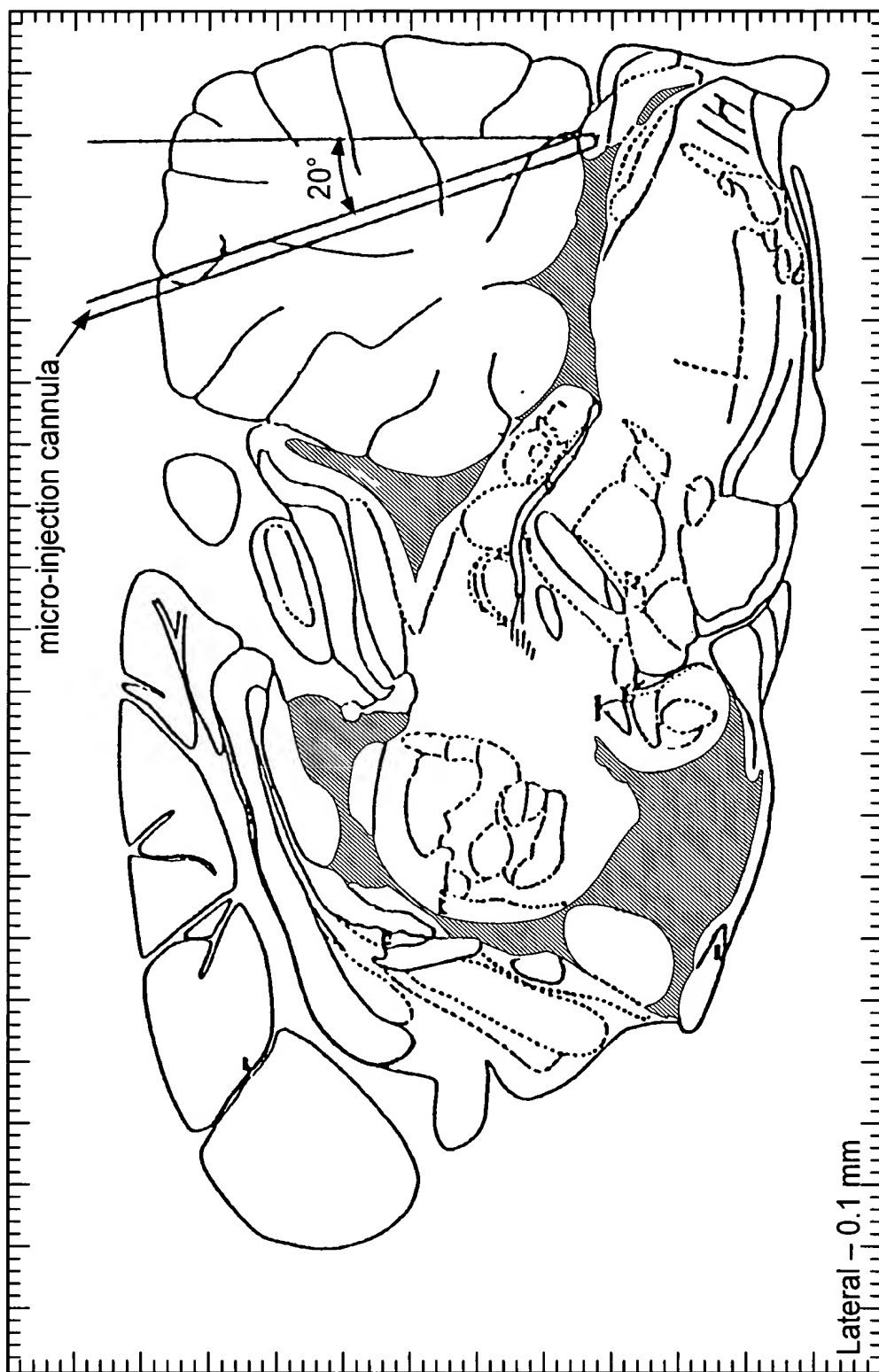


FIG. 46

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direct blood pressure

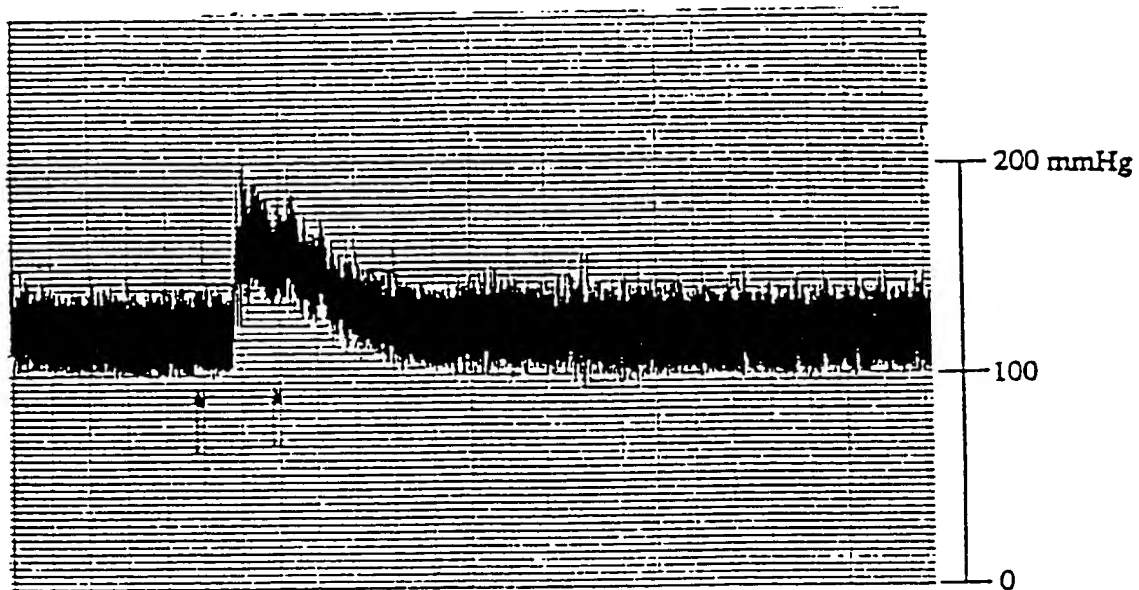


FIG. 47A

mean blood pressure

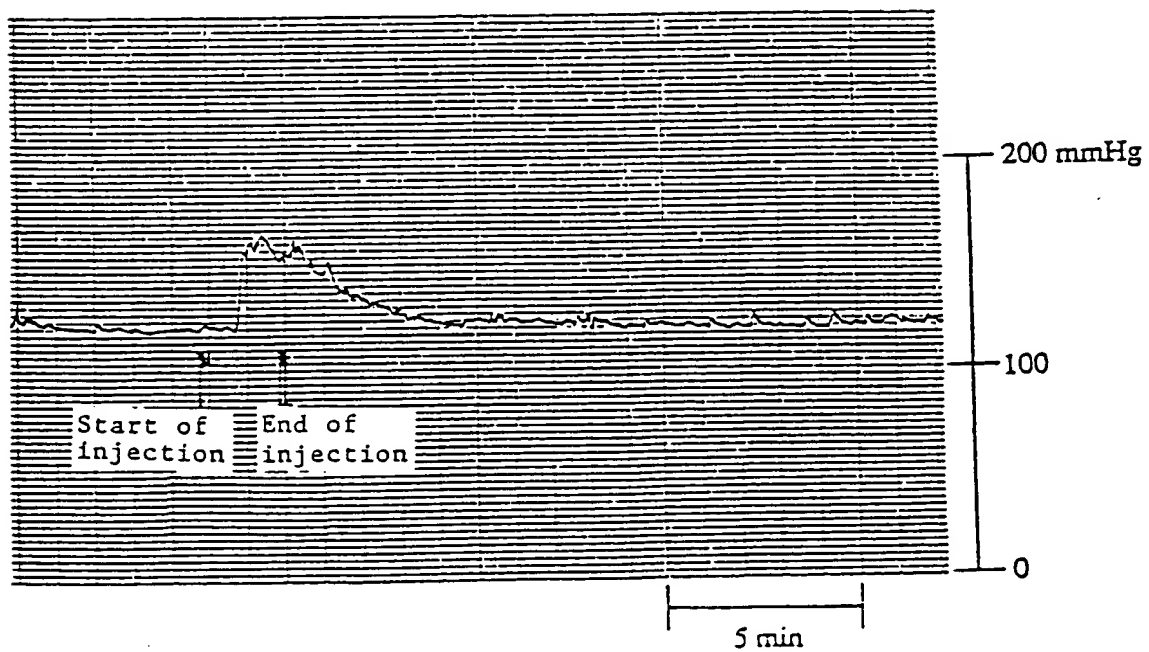


FIG. 47B

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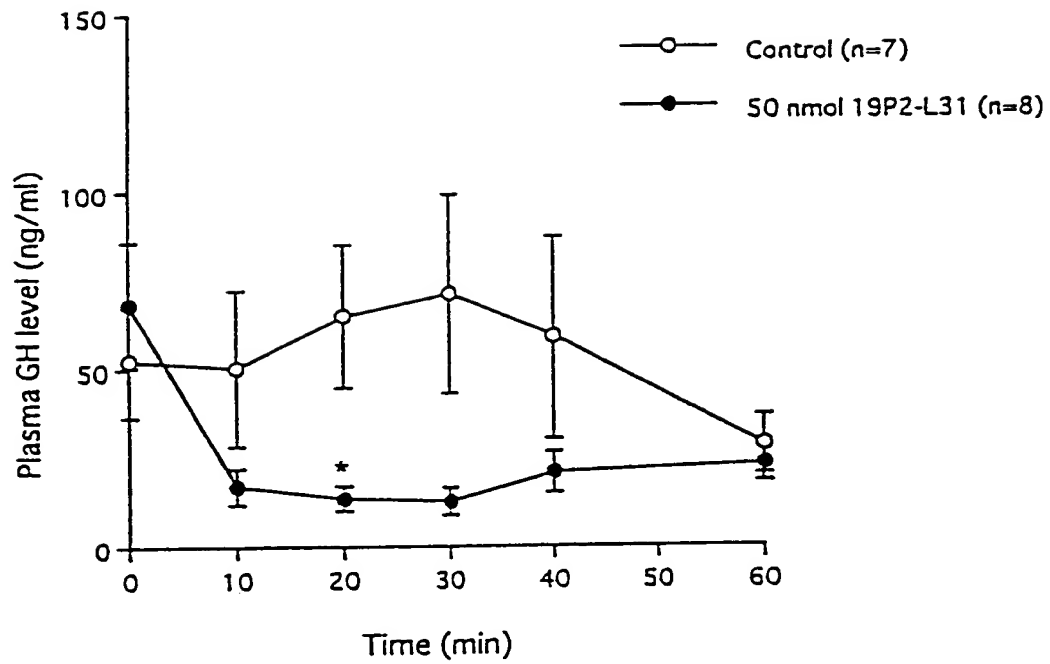


FIG. 48

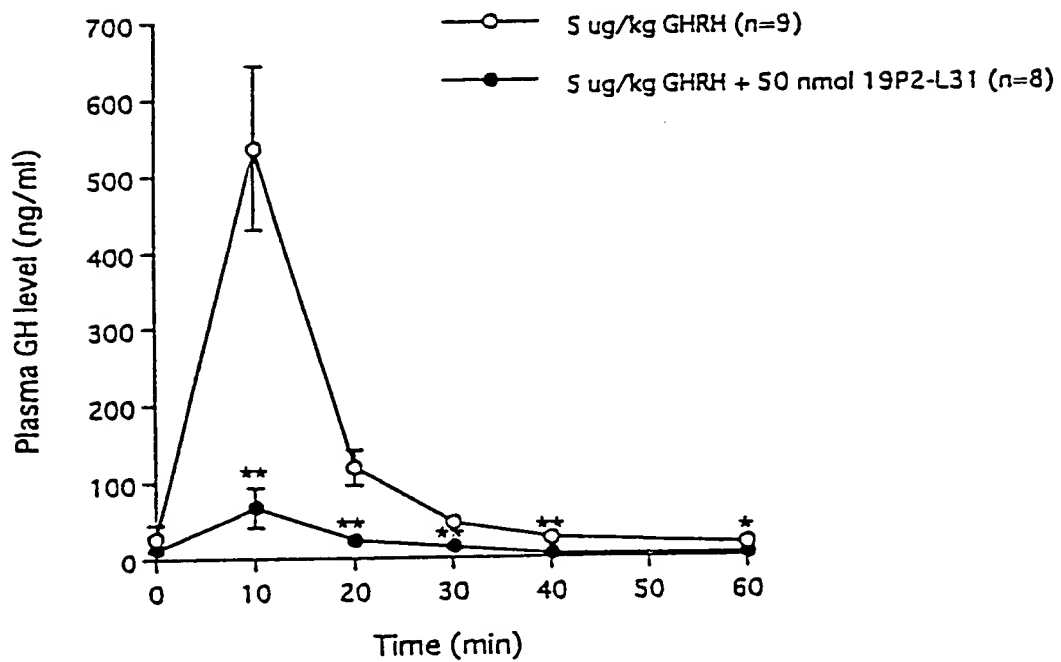


FIG. 49

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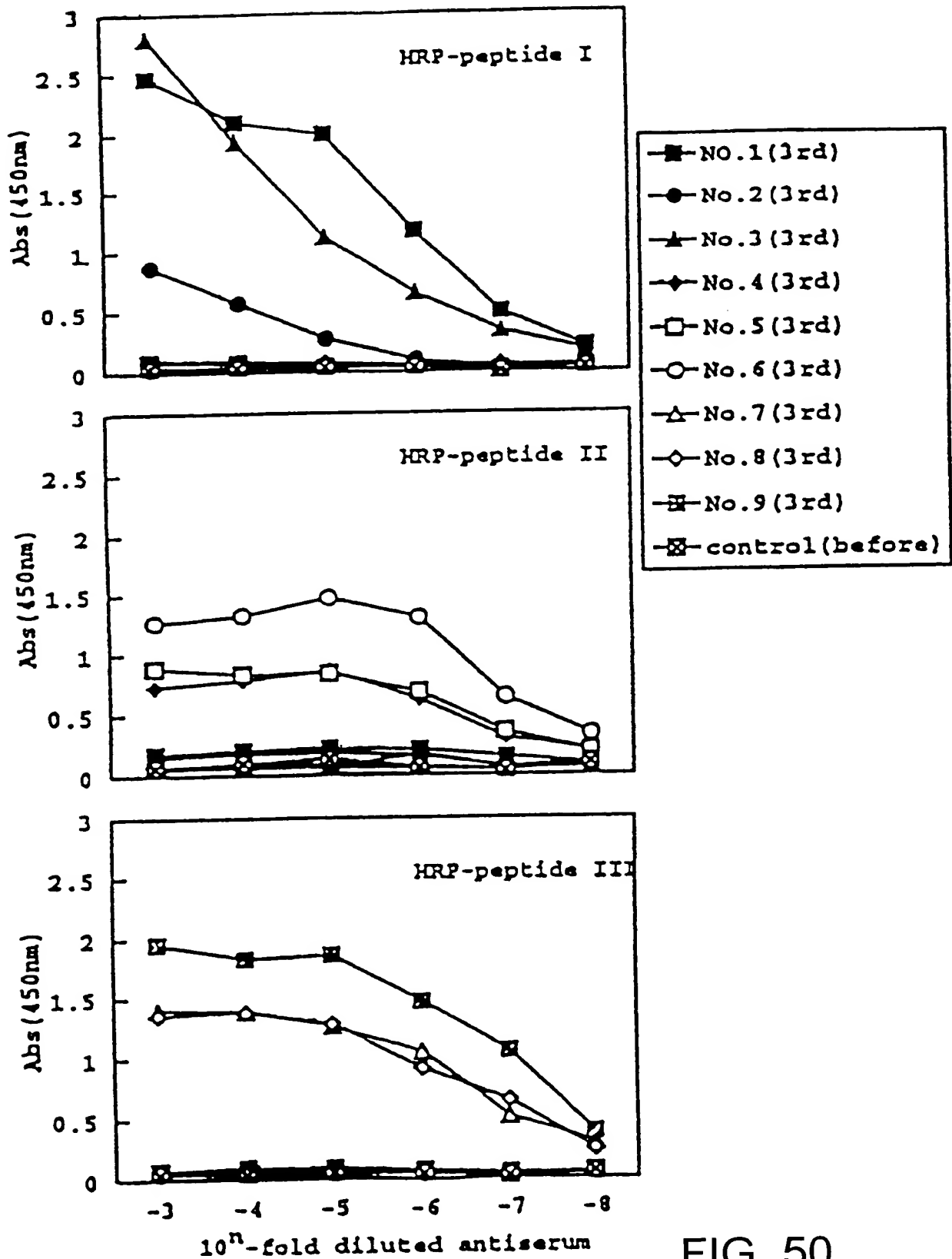


FIG. 50

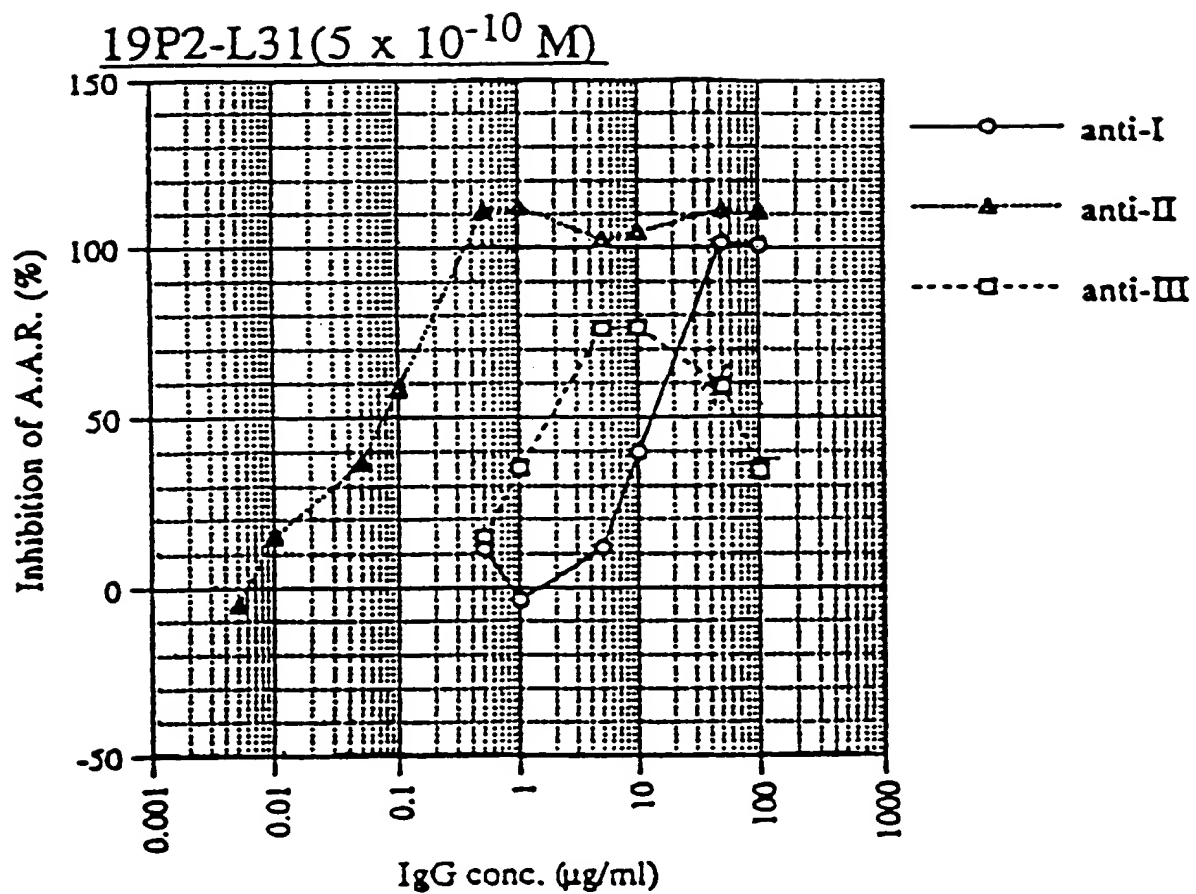


FIG. 51





FIG. 52A
FIG. 52B
FIG. 52C
FIG. 52D
FIG. 52E

FIG. 52A  
FIG. 52

5'	9	18	27	36	45	54
ATG ACC TCA CTG CCC CCT GGA ACC ACT GGG GAC CCC GAT TTG TTT TCT GGG CCG						
---	---	---	---	---	---	---
Met Thr Ser Leu Pro Pro Gly Thr Thr Gly Asp Pro Asp Leu Phe Ser Gly Pro						
63	72	81	90	89	108	
TCG CCA GCC GGC TCC ACT CCA GCC AAC CAG AGT GCA GAG GCT TCA GAG AGC AAT						
---	---	---	---	---	---	---
Ser Pro Ala Gly Ser Thr Pro Ala Asn Gln Ser Ala Glu Ala Ser Glu Ser Asn						



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117	126	135	144	153	162
GTG TCT GCG ACG GTT CCC AGA GCT GCA GCA GTC ACG CCG TTC CAG AGC CTG CAA					
---	---	---	---	---	---
Val Ser Ala Thr Val Pro Arg Ala Ala Val Ala Val Thr Pro Phe Gln Ser Leu Gln					
171	180	189	198	207	216
CTA GTG CAC CAG CTG AAG GCA CTG ATC GTG ATG CTG TAC AGC ATC GTG GTG GTC					
---	---	---	---	---	---
Leu Val His Gln Leu Lys Ala Leu Ile Val Met Leu Tyr Ser Ile Val Val Val					
225	234	243	252	261	270
GTG GGT CTG GTG GGC AAC TGC CTT CTT GTG CTG ATC GTG CGC GTG CGC CGG					
---	---	---	---	---	---
Val Gly Leu Val Val Gly Asn Cys Leu Leu Val Val Ile Ala Arg Val Arg Arg					
279	288	297	306	315	324
CTG CAC AAC GTG ACC AAC TTC CTC ATC GGC AAC GGC CTG GCC TTC TCC GAT GTG CTC					
---	---	---	---	---	---
Leu His Asn Val Thr Asn Phe Leu Ile Gly Asn Leu Ala Leu Ser Asp Val Leu					
333	342	351	360	369	378
ATG TGT GCC GCC TGT GTG CCT CTC ACG CTG GCC TAC GCC TTT GAA CCT CGT GGC					
---	---	---	---	---	---
Met Cys Ala Ala Cys Val Pro Leu Thr Leu Ala Tyr Ala Phe Glu Pro Arg Gly					

FIG. 52B

387	405	414	423	432
TGG GTG TTC	GGT GGA GGC CTG TGC CAC CTT GTT TTC	CTG CAG CCG GTC ACC		
---	---	---	---	---
Trp Val Phe	Gly Gly Leu Cys His Leu Val Phe	Leu Gln Pro Val Thr		
441	450	468	477	486
GTC TAC GTA	TCG GTG TTC ACA CTC ACC ACA ATC GCT GTG GAC CGC TAT GTG GTT			
---	---	---	---	---
Val Tyr Val	Ser Val Phe Thr Leu Thr Thr Ile Ala Val Asp Arg Tyr Val Val			
495	504	513	522	531
CTG GTG CAC	CCG CTA CGT CGG CGC ATT TCA CTG AAG CTC AGC GCC TAC GCT GTG			
---	---	---	---	---
Leu Val His	Pro Leu Arg Arg Arg Ile Ser Leu Lys Leu Ser Ala Tyr Ala Val			
549	558	567	576	585
CTG GGC ATC	TGG GCT CTA TCT GCA GTG CTG GCG CTG CCG GCC GCG GTG CAC ACC			
---	---	---	---	---
Leu Gly Ile	Trp Ala Leu Ser Ala Val Leu Ala Leu Pro Ala Ala Val His Thr			
603	612	621	630	639
TAC CAT GTA	GAG CTC AAG CCC CAC GAC GTG GCG CTC TGC GAG GAG TTC TGG GGT			
---	---	---	---	---
Tyr His Val	Glu Leu Lys Pro His Asp Val Arg Leu Cys Glu Glu Phe Trp Gly			

FIG. 52C



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657	666	675	684	693	702
TCG CAG GAG CGC CAG CGA CAG ATC TAT GCC TGG GGG CTG CTG GGC ACC TAT					
---	---	---	---	---	---
Ser Gln Glu Arg Arg Gln Arg Gln Ile Tyr Ala Trp Gly Leu Leu Gly Thr Tyr					
711	720	729	738	747	756
TTG CTC CCC CTG CTG GGC ATT CTC CTG TCT TAC GTC CGG GTG TCG GTG AAG TTG					
---	---	---	---	---	---
Leu Leu Pro Leu Leu Ala Ile Leu Leu Ser Tyr Val Arg Val Ser Val Lys Leu					
765	774	783	792	801	810
CGG AAC CGC GTG GTG CCT GGC AGC GTG ACC CAG AGC CAG GCT GAC TGG GAC CGA					
---	---	---	---	---	---
Arg Asn Arg Val Val Pro Gly Ser Val Thr Gln Ser Gln Ala Asp Trp Asp Arg					
819	828	837	846	855	864
GCG CGT CGC CGT CGC ACT TTC TGC CTG CTG CTG GTG GTG GTG GTG TTC GCG					
---	---	---	---	---	---
Ala Arg Arg Arg Arg Thr Phe Cys Leu Leu Val Val Val Val Val Phe Ala					
873	882	891	900	909	918
GTC TGC TGG CTG CCT CTG CAC ATT TTC AAC CTG CTG CGG GAC CTG GAC CCG CGT					
---	---	---	---	---	---
Val Cys Trp Trp Leu Pro Leu His Ile Phe Asn Leu Leu Arg Asp Leu Asp Pro Arg					

FIG. 52D



927	GCC ATC GAC CCC TAC GCC	936	TTC GGG CTG GTG CAG CTC	954	CTC TGC CAC TGG CTT	972	GCC
---	---	---	---	---	---	---	---
Ala Ile Asp	Pro Tyr Ala Phe Gly Leu Val Gln Leu Cys His Trp						Ala
981	ATG AGC TCC GCC TGC TAC AAC CCC TTC ATC TAT GCG TCG CTG CAC GAC AGC	990	999	1008	1017	1026	TTC
---	---	---	---	---	---	---	---
Met Ser Ser Ala Cys Tyr Asn Pro Phe Ile Tyr Ala Ser Leu His Asp Ser							Phe
1035	CGA GAG GAG CTA CGC AAG ATG CTT CTG TCT TGG CCC CGC AAG ATC GTG CCT	1044	1053	1062	1071	1080	CAT
---	---	---	---	---	---	---	---
Arg Glu Glu Leu Arg Lys Met Leu Leu Ser Trp Pro Arg Lys Ile Val Pro							His
1089	GGC CAG AAT ATG ACC GTC AGT GTG GTC ATC TGA	1098	1107	1116			
---	---	---	---	---	---	---	---
Gly Gln Asn Met Thr Val Ser Val Val Ile							1'

FIG. 52E